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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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is the number of results predicted by chance to have a Pred. No.

Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 24 25-OCT-2001;

REFERENCE AUTHORS TITLE JOURNAL

AX350512 Sequence
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AF264095 Homo sapi
AL158163 Homo sapi
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AX350513 Sequence
AF316894 Homo sapi
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M18415 Human plate
J05652 Porcine alp
U25722 Cavia porce
U79031 Rattus norv
M6377 Rat alpha-2
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AF281308 1353 bp DNA linear PRI 05-DEC-2000
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1 (bases 1 to 1353)
Small_A.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
An asn to 1ys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
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Small, K.M., Forbes, S.L., Bridges, K.M. and Liggett, S.B.
Direct Submission
Submitted (22-UNN-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
Location/Qualifiers
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/product="alpha 2A adrenergic receptor"
/protein_id="AAF91441.1"
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/db_xref="taxon:9606"
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KAWCSTPYLALDVLFCTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVNGYWYFG
SAVISPPLISIEMEKTAIITTWVI
SAVISPPLISIEMEKGGGGPQPAEPKCEINDOKWYISSCIGSFPAPCLIMLLVVVN
IYQIAKRRTRVPPSRRGPDAVAPPFGGTERRPNGLGPERSAGPGGAEAEPLPTQLNGA
PGEPPAAPGRYDTDALDLEESSSSDHARERPGFRFRERQPRGKGRARARQVRGDSLPR
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Castellano, M., Giache', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.
A search for genetic variability in the human alpha-2 adrenergic receptor on chromosome 10
Unpublished
E. Chases I to 191)
Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.
Direct Submission
L. Submitted (29-APR-2000) Medical and Surgical Sciences, University of Brescia, Spedai Civili di Brescia, Brescia, 125100, Italy Schaper 1 to 1941)
E. Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Direct Submission
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                                                                                                CAGGCGAGCGGCTCCAGGGCCCCGCAGACCCGAGCGCGGTCCCCGGGGCAAAGGCAAG
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RGPGATGIGTPAAGEGERVCAAKASWRGRONEEKRFTFVLAVVIGYFVVCWRPFFF
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                                /note="compared to sequence described in Bono et
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/replace="9"
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/codon_start=1
/product="adrenergic receptor alpha-2A"
/protein id="AAG00441.2"
/db_xref="G1:9864782"
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e, Fucheng Road No. 30, Beijing 100036,
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Bukaryogis.

Bukaryogis.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3612)

Liu,L. and Yuan,L.

Human alpha-2A adrenergic receptor gene and the genotype of -1296

Unpublished

2 (bases 1 to 3612)

Liu,L. and Yuan,L.

Liu,L. and Yuan,L.

Direct Submission

Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
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Homo sapiens alpha-2A adrenergic receptor (ADR2AR)
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/db_xref="taxon:9606"
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3 (bases 1 to 3653)
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5 (bases 1 to 3654)
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1. 3653
6 (cranion/Qualifiers
7 (crganism="Homo sapiens"
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1 (bases 1 to 3653)
Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
Clohing and expression of human alpha-2A adrenergic receptor in SY5Y cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA linear PRI 27-M
receptor mRNA, complete cds
             2925 GCGCCGGCCCGCGCGCGCACACCGACGCTGGACCTGGAGGAGAGACTCGTCTTCCGAC
                                                                                                                                                                                                              3105 GGGATCGGGACGCCGGCTGCAGGGCCGGGGGAGGAGCGCGTCGGGGCTGCCAAGGCGTCG
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CAGATCGCCAAAGCGTCGCACCCGCGTGCCACCCAGCCGCCGGGGGTCCGGACGCCGTCGCC
                                               GCGCCGCCGGGGGGCACCGAGGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGGC
                                                               CCGGGGGGCGCAGAGGCCGAACCGCTGCCCAGCTCAACGGCGCCCCTGGCGAGCCC
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Homo sapiens
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AF284095
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DEFINITION
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Direct Submission

Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Direct Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CEUN (18A, UK. E-mail enquiries: Cambridgeshire, CEUN (18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Dec 5, 2001 this sequence version replaced gli16944657.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amoration may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
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Liggett, S.B. and Small, K.M.
Liggett, S.B. and Small, K.M.
Patent: WO 0179561-A 25 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M.
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/organism="Homo sapiens"
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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP thtp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10. Constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at http://www.aanger.ac.uk/HGP/Chri0
RPII-148NS is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                               DB 6; Length 1350;
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                                               Score 1348.4; DB 6
Pred. No. 3.6e-159;
0; Mismatches 1;
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    /db_xref="taxon:9606"
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1 (bases 1 to 1353)
Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced
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Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
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Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
Direct Submission
Submitted (26-OCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
Location/Qualifiers
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J. Biol. Chem. 275 (49), 38518-38523 (2000)
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/db_xref="taxon:9606"
/chromosome="10"
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/gene="ADRA2A"
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/gene="ADRA2A"
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/map="10q23-q25"
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/note="compared to wild type sequence presented
Accession Number 45281308; polymorphic sequence
Lys at amino acid 251"
/frequency="Caucasians 0.004; African-Americans
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Pred. No. 3.6e-159;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 3604)

Fraser_C_M_, Arakawa,S., McCombie,W.R. and Venter,J.C.

CIoning, sequence analysis, and perimanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.

Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation

1. Biol.

89308571
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Location/Qualifiers
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adrenergic receptor; alpha-2 andrenergic receptor.
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LLTVFGNVLVIIAVFTSRALKAPQNLFUVSLASADILVATLVUTPFSLANDYNGYWYPG
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SAVISPPALISTEKKGGGGOPQPAEPRCBINDQKWYVISSCIGSFFACCLIMILVVVN
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AGGBPAPARGARDTDALDLESSSSCHABREPPGGRRGKGRARASQVKFGDSLRG
AGRGRRGSGRRLQGGRRSASGLPRRRAGAGGNREKRFTFVLAVVIGVFVVVVWFPFFF
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Homo.

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Cataria, M.C., Lefkowitz,R.J. and Regan,J.W.

Clanon, M.C., Lefkowitz,R.J. and Regan,J.W.

Cloning, sequencing, and expression of the gene coding for the human platelet alpha 2-adrenergic receptor

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PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
J05652
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1 (Dases 1 to 1728)

Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J.Jr. and Limbird, L.E.
Unpublished (1990)

2 (bases 70 to 1582)
                                                                                                                                                                                       2 (bases 70 to 1582)
Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cragoe, E.J. and Limbird, L.E.
Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Nf. H+, and amiloride analogs
J. Biol. Chem. 265 (28), 17307-17317 (1990)
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Location/Qualifiers
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Porcine liver DNA.
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Best Local Similarity 99.5%; Pred. No. 1.6e-155;
Matches 1344; Conservative 0; Mismatches 5; Indels
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1. .2291

/organism="Cavia porcellus"

/strain="Sasco Hartley albino"

/db xref="taxon:10141"

/clone="(GP) alpha-2A"

49. .1401
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KANCEIVLALDVLFCTSSIHLGAPQNNFLVSLASADILVATLVIPFGLANBVNGYWYFG
KANCEIVLALDVLFCTSSIHLGAPGGQQPAEPRCEINOGWYVISSCIGSFFAPCLINILVYW
IYQIAKRRTRVPPSRRGPDAAALFGGAERRPNGLGPBRGVGRVGABAEPLVQLNGA
PGGPAPAGRDADGLDLESSSSEHARPRPPGRSENGPRAKSRARASQVKPGDSLPR
RGPGAPGGBRGARAGSRWRGRQNREKKFTFVLAVUGVFVVVCMFPFF
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2 (bases 1 to 2291)
Richman, J.G.
Direct Submission
Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA
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Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
1 (bases 1 to 2291)
Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
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Venkataraman, V., Duda, T.M. and Sharma, R.K.
Direct Submission
Submitted (20.NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA
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Wypijewski,K., Duda,T. and Sharma,R.K.
Structural, genetic and pharmacological identity of the rat al
2-adrenergic receptor subtype ca2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
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Chalberg, S.C., Duda, T., Rhine, J.A. and Sharma, R.K.
Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Rattus norvegicus alpha2D adrenergic receptor mRNA,
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TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYITIFNHDFRRAFKKILCRGDRKRIV
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            /product="alpha-2A adrenoceptor"
/protein_id="AAA67074.1"
/db_xref="GI:818875"
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LFTVFGNVLVIIAVFTSRALKAPQNNETVSLASDLIVATIVIPFSLANEWNGYWYFG
KVWCEYLLADUVLFCTSSITULGISLDRYWSITQAIEYNLKRTPRRIKATIVTVWYI
SYJSPPLISIDKGAGGGQDPAEPGCKINDQKWYUSSSGSFFAPCLIMILVYYW
IYQIAKRRTRVPPSRRGPDAGSAPFGGADRRPNGLGFBRGAGTAGABAEPLFFQLNGA
RGBAPPRRADGDALDLESSSSSEHARPRQFGGRERAGTAGABAEPLFFTQLNGA
RGPGAAGGGGGERAGGGRARASWRGGNREKRFTFVLANVIGYFVVVCWFPFFF
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Pred. No. 4.4e-129;
0; Mismatches 152; Indels
                                                                       receptor'
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                                                                                                                                                                                              306
                           /strain="Sprague-Dawley/db_xref="taxon:10116"
Location/Qualifiers
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Best Local Similarity 88.7%;
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Isolation of rat genomic clones encoding subtypes of the alpha
Ladrenergic receptor. Identification of a unique receptor subtype
J. Biol. Chem. 266 (16), 10470-10478 (1991)
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Rattus norvegicus (strain Sprague-Dawley) adult liver
Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/db xref="taxon:10116"
/tissue_type="liver"
/dev stage="adult"
1. [1353]
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1140 1200 1260

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1 (bases 1 to 2923)
Venkaturaman,V., Duda,T. and Sharma,R.K.
The bovine alpha 2D-adrenergic receptor gene: structure, expression
in retina, and pharmacological characterization of the encoded
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Bos taurus
Bukaryotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Venkataraman, V., Duda, T.M. and Sharma, R.K.
Venkataraman, V., Duda, T.M. and Sharma, R.K.
Subrict Submission
Submitted (10-000-1996) Cell Biology, UMDNJ-SOM, 2 Medical
Stratford, NJ 08084, USA
Location/Qualifiers
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   1021 GGCCGGGGGCTCGGGGCTCCGGGGAGGGAGCGTGCCGGGGGGCGCCCAAAGCGTCG
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Bos taurus alpha2D adrenergic receptor gene, complete cds.
U79030
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RGPGAAGPGGGERAAGSWRGGNRERFFTVLAVUGVFVVCWFPFFF
IYTLIAVGCPVPYQLFNFFWFGYCNSSLNPVIYIIFNHDFRRAFKKILCRGDRKRIV
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                                                                                                                                                                                                                                                                              Score 1095.6; DB 10; Length 1380;
Pred. No. 1.1e-127;
0; Mismatches 159; Indels 0;
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                             'gene="RG20"
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Best Local Similarity 88.2%;
Matches 1191; Conservative
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FFTYTLTAIGGPVPPTLFFFFFWFGYCNSSLNPVIXTIFNHDFRRAFKKILCRGDRKR
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Pred. No. 1.2e-127;
0; Mismatches 125;
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                                    2349 GAGCCCGCGCCCCCAGGCGC---CGGAGCCGACGCGCTGGACCTAGAGGAGAGCTCCTCG
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Search completed: March 11, 2003, 00:54:24 Job time : 20288.5 secs

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1509. 2867
Codon strattel
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FFTYTLTAIGCPVPPTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKR
                                                                      Venkataraman, V., Duda, T.M. and Sharma, R.K.
Venkataraman, V., Duda, T.M. and Sharma, R.K.
Direct Submitsaton
Submitred (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr Dr,
Stratford, NJ 08084, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.5%; Score 33; DB 4; Length 2923; 87.8%; Pred. No. 2.4;
Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)
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1509. .2867
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Bos taurus alpha2D adrenergic receptor gene, complete cds.
U79030
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Bovinae; Bovinae; Bos.
1 (bases 1 to 2923)
Venkataraman, V., Duda, T. and Sharma, R.K.
The bovine alpha 2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor
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96682. 105311_
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Best Local Similarity 90.2<sup>1</sup>
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                    Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Calangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dearx, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gordte, M., Gaden, J., Gardyna, S., Ginde, S., Gordte, M., Gaden, J., Gardyna, S., Ginde, S., Gordte, M., Illev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macclean, C., Macchan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Cannon, J., Zambek, L., Zimmer, A. and Zody, M., Subrams, M., Subrams, R., Travere, M., Travis, D., Ye, W.J., Young, G., Churles, M., Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Churles, M., Subrams, M., Subrams, R., Alles, A., Millson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Churles, M., M., Subrame, A., Talamas, J., Tesfaye, S., Theodore, J., Direct, Submission, M., Submer, A., And Zody, M., 
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Lubmitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Contun, A., R., & Green, P. (Babridge, MA) 02141, USA

On Jun 6, 2002 this sequence version replaced gi:21313866.

All repeats were identified using Repeatmasker:
                                              Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Center: Whitehead Institute/ MIT Center for Genome Research
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------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-358H2
Unpublished
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**NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**This sequence will be preserved.

**This sequence as soon as it is available and the accession number will be preserved.

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                                                                                                                                  Insert size: 210000; agarose-fp
Insert size: 202017; sum-of-contigs
Quality coverage: 6.3 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs
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98682 105311: contig of 6630 bp in length
105312 105411: gap of 100 bp
105412 122788: contig of 17377 bp in length
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122889 132289: contig of 9401 bp in length
132290 132389: gap of 100 bp
132390 144818: contig of 12429 bp in length
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177389 201231: contig of 23843 bp in length
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144919 159101: contig of 14183 bp in length
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27175: contig of 3072 bp in length
775: gap of 100 bp
3056: contig of 3286 bp in length
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Consensus quality: 197709 bases at least Q40 Consensus quality: 200412 bases at least Q30 Consensus quality: 201149 bases at least Q20
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15172: contig of 2195 bp in length
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18061: contig of 2789 bp in length
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1. .7387
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AC113491/c
                                                                                                                                                                  DEFINITION
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                                                                                                                 RESULT 13
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Rattus norvegicus alpha2D adrenergic receptor mRNA, complete cds.
U79031
RGPGAAGPGASGSGHGEERGGGAKASRWRGRQNREKRFTFVLAVVIGVFVVCWPPFFF
TYTLIAVGCPVPSQLFNFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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SAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFFAPCLIMILVYVR
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BERPARTRAPRODALDLEBSSSSBEHARRPQGPKFBRGPRAKGKTKASQVKPGDSLPR
RGPGAAGPGASGSGGERAGARASRWRGRQNREFFTFVLAVVIGVFVVCWFPFFF
TYTLIAVGCPVPYQLFNFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRRRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wypijewski.K., Duda,T. and Sharma,R.K.
Wypijewski.K., Duda,T. and Sharma,R.K.
Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype 6A2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Venkataraman, V., Duda, T.M. and Sharma, R.K.
Venkataraman, V., Duda, T.M. and Sharma, R.K.
Venkataraman, V., Duda, T.M.
Submission
Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA
Location/Qualifiers
                                                                                                                                                 Gaps
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                                                                                                             Length 1454;
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                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                     780 GGGGGCGCGATCGCAGGCCCAACGGGTGGGCCCGGAGCG 820
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Mol. Cell. Biochem. 144 (2), 181-190 (1995)
95349560
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/db_xref="taxon:10116"
1. 71353
                                                                                                             DB
                                                                                                           Score 34.6; DB
Pred. No. 0.94;
0; Mismatches
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Best Local Similarity 90.2%;
Matches 37; Conservative
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Matches 37; Conservative
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Gaps

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SAVISPPPLISIEKKAGGGGQQPAEPRCEINDOKWYVISSCIGSFFAPCLIMILVYVR
                                                                                                                                                              PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
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BEBAPAGRADADGLDLEESSSSEHAERPPGPRRSERGPRAKSKORASQVKPGDSLPR
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TYTLTAVGCSVPPTLFKFFPWFGYCNSSLNPVIYTIPNHDFRRAFKKILCRGDRKRIV
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Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
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2 (bases 70 to 1582)
Guyer, C.S. A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cragoe, E.J. Jr. and Limbird, L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+, H-, and amiloride analogs J. Biol. Chem. 265 (28), 17307-17317 (1990)
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
[ (bases 1 to 1728)
Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J.Jr.
and Limbird, L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) In press) kindly submitted by C.A.Guyer, 02-40G-1990.
Location/Qualifiers
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Pred. No. 0.91;
0; Mismatches 4; Indels 0:
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730 GGGGGCCCGATCGCAGCCCAACGGGCTGGGCCCGGAGCG 770
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AC113491.3 GI:21327601
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus
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130. .1482
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alpha-2A-adrenergic receptor.
Porcine liver DNA.
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Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                       IYQIAKRRTRVPPSRRGPDAVAAPPGGTERRPKGLGPERSAGPGGARAEPLPYQLNGA
PGEPAPAGREDTDALDLEESSSSDHAERPPGPRRCPRGFRGKGKARASQVKPGDSLPR
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/note="compared to wild type sequence presented in GenBank
Accession Number AF281308; polymorphic sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROD 27-APR-1993
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukampalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1454)
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Mol. Pharmacol. 42 (1), 16-27 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lys at amino acid 251"
/frequency="Caucasians 0.004; African-Americans 0.05"
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                                  'product="alpha 2A adrenergic receptor"
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Mouse alpha-2 adrenergic receptor, complete cds.
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/strain="129/Sv"
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alpha-2 adrenergic receptor.
Mus musculus (strain 129/Sv) DNA.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordates, Catarrhini, Hominidae, Homo.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Masses 1 to 1353)
Masses 1 to 1353)
An ann to 135 polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced
Masoniet-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
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Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
Direct Submission
Submitted (26-GCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
Location/Qualifiers
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Alpha-2 adrenergic receptor polymorphisms
Patent: Wo 0.179561-A 25 S-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="10"
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/db_xref="taxon:9606"
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/gene="ADRA2A"
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ilarity 97.6%;
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Direct Submission

AL Cambridgeshire, CB10 184, UK. E-mail enquiries:

Cambridgeshire, CB10 185, UK. E-mail enquiries:

Cambridgeshire, CB10 185, UK. E-mail enquiries:

humquer/@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

buring sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempte was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw:

SMISSPROT; Tr., TREMBL; Wp., WORNDEP; Information on the WORNDEP,

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 10, constructed by the Sanger Centre Chromosome 10

http://www.sanger.ac.uk/HGP/Ch110

RP11-348NS is from the library RPC1-11.2 constructed by the group

of Piecer de Jong. For further here

of Piecer de Jong. For further here

http://www.sanger.ac.uk/HGP/Ch10

of Piecer de Jong. For further here

of Piecer de Jong. For further here
          TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
                                                                                                                                                                                                                                                                                                                                                                                           AL158163 204908 bp DNA linear PRI 13-DEC-2001
Human DNA sequence from clone RPI1-348N5 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11.2"
62115 a 36724 c 39536 g 665
                                                       1028 g
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AL Unpublished
AE Unpublished
AB Ao.2.-W. Tang, K., Li, B.-M. and Jing, N.-H.
B Direct Submission
ACAdemy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
Location/Qualifiers
Location/Qualifiers
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
Location/Qualifiers
                                                                                                                                                                                      3653 bp mRNA linear PRI 27-MAR-2001
Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
AF284095
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KAWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIITVWVI
SAVISPPDLISIEKKGGGGGQPQPAEPRCEINDQKWYJSSCIGSFFAPCLIMILVYW
IYQIAKRRTRVPPPSREGDAVAPPGGTERRPNGLGPERSAGPGABAEPLFTQLNGA
PGEPAPAGPRDDALDLEESSSSDHARRPPGRPRRPERGGRAGOVRFQCNGR
RGPGATGIGTPAAGPGEERVGAAKASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFF
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3653)
Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
Cloning and expression of human alpha-2A adrenergic receptor in
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                                                                                                                         'product="alpha-2A adrenergic receptor"
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/producte="alpha-2A adrenergic receptor"
/protein_id="MAK26743.1"
/db_xref="G1:33447751"
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/cell_line="SY5Y"
880. .2232
/map="10q23-q25"
<2085. .>3437
/gene="ADR2AR"
                                                                         <2085. .>3437
/gene="ADR2AR"
                                                                                                                                                                    'gene≂"ADR2AR"
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ilarity 100.0%;
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Best Local Similarity
Matches 41; Conserv
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AF284095
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/ DECCETIA 1178196"

/ db_xref="d1:178196"

/ db_xref="d1:178196"

/ talsolation="WGSLQPDAGNASWNGTBAPGGGARATPYSLQVTLTLVCLAGLLM
/ translation="WGSLQPDAGNASWNGTBAPGGGARATPYSLQVTLTLVCLAGLLM
LLTVFGNVLV11AVFTSRALKAPQNLFLVSLASADILWATLV1PFSLAMFNTFVYFG

KAMCBIYLALDVLFCTSSTTHLCAISLENEWWSTTYDAISVNLKRTPRRIKATIITVWVI
SAVISFPPLISIEKKGGGGPQPABFRCEINDQKWYVISSCIGSFFAPCLIMILVVVN
IYQIAKRRTRVPPSRRGPDAVAAPGGGTERPROTGPBRAGPGGARABELFTQLMGA
PGERPAPAGROTDTALLINESSSSCHARRPPGGFRRPRGFRGAGRAGGARABELFTQLMGA
AGRGRRGGGRRADGAGRASSSSCLPRRRAGAGGONREKRFTFVLAVVTGVFVVCWFPFFF
TYTLTAVGGSCPRLDFKFFFWFGYCNSSLNPVITIFNHDFRRAFKKILCRGDRKRIV
                                   2568356
Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McCombie, 30-MAR-1989.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha-2 adrenergic receptor old gene name 'ADRA2R'"
/codon_start=1
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General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
China
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Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3612)
Liu,L. and Yuan,L.
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/note="glucocorticoid response element"
1723. 1728
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'note="GRE related sequence"
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                                                                                                                 1. .3604
/organism="Homo sapiens"
/db xref="taxon:9606"
/map="10q23-q25"
1578. .1583
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/chromosome="10"
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AY032736.1 GI:14029162
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/gene="ZNF32"
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/gene="ZNF32"
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Liu, L. and Yuan, L.
Direct Submission
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Homo sapiens
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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Cararrhini; Hominidae; Homo.

1 (bases 1 to 3604)
Frasesr.C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
Fraserr.C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.

Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation
Gyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="compared to sequence described in Bono et al, Gene
Geography 10:151-160, 1996"
                                                                                                                                       Castellano, M. Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.

Direct Submission

L Submitted (19-APR-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy of Brescia, Spedali Civili di Brescia, Brescia, Spedali Civili di Brescia, Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy Scatellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.

Direct Submission

L Submitted (22-AUG-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy Sequence update by submitter

On Aug 22, 2000 this sequence version replaced gi:9837145.
                                                                                                                                                                                                                                                                                                                                        University
                                                                                                                                                                                                               University
Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E. A search (or genetic variability in the human alpha-2 adrenergic receptor on chromosome 10 Unpublished
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/protein_id="AAG00447.2"
/db_xref="GI:9864782"
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Organism="Homo sapiens"

/db_xref="texon:9606"

/chromosome="10"

/map="10q24-q26"
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M23533.1 GI:178195
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Human platelet alpha-2-adrenergic receptor gene, complete cds.
M18415
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Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
AF262016
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BERPRAGRENDTDALDLEESSSSDHRARPPGPRRPERGRGKGKARAGOVKPGDSLRG
AGRGRRGSGRRLQGRGRASGLPRRAGAGGGNLEKRFTFVLAVVIGVFVVCWPPFFF
TYTLTAVGSVPRTLEKFFFWRGYCNSSLNVVIYTIPHDFRRAFKKILCRGBRKRIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha-2-adrenergic receptor old gene name 'ADRA2R'"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1941)
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Human (lambda-EMBL 3 library) DNA.
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/map="10q23-q25"
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Chromosome 10q23-q25.
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LLTVFGNVLYIIAVFTSRATARAPQNLFLVSLASADILVATLVTPFSLANEVMGYWYFG
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SAVISPPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCIGSFFAPCLIMILVYVR
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FREPRAGREPTUTALDLEESSSSDHARRPPGPRRPERGPRGKGKARASQVKRGDSLPR
RGPGATGIGTPAAGEERVGARASRWRGRONREKRFTFVLAVVIGVFVVCWPPFFF
TYTLTAVGCSVPRTLFKFFFWPGYCNSSLNPVIYIIFNHDFRRAFKKILCRGDRKRIV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1353)
Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
3. Biol. Chem. 275 (49), 38518-38523 (2000)
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Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
Direct Submission
Submitted (22-UTM-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   Length 1350;
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protein id="AAF91441.1"
'db_xref="GI:9652210"
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/note="G-protein coupled receptor"
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                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 6; 100.0%; Pred. No. 0.012;
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Pred. No. 0.012;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
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/gene="ADRA2A"
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Matches 41; Conservative
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FEATURES

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March 10, 2003, 18:28:11; Search time 607.543 Seconds (without alignments) 1964.002 Million cell updates/sec
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Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                           nucleic search, using sw model
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Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

AX350512.1 GI:18616107

human.

Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 24 25-OCT-2001;

REFERENCE AUTHORS TITLE JOURNAL

U79031 Rattus norv J05622 Portine alp AC113491 Mus muscu U79030 Bos taurus MC3722 Cavia porce AX344974 Sequence AX344895 Sequence AX344895 Sequence AX090342 Homo sapi AC105677 Rattus no AE002058 Deinococc AL109663 Streptomy AL356300 Homo sapi AC12524 Homo sapi AC12706 Homo sapi AC112706 Homo sapi PAT 06-FEB-2002 AL158163 Human DNA AX350513 Sequence AF316894 Homo sapi M99377 Mouse alpha Sequence Sinorhizo Rhizobium Homo sapi Homo sapi Homo sapi Homo sapi M23533 Human alpha AY032736 Homo sapi AF284095 Homo sapi Rattus no BC004261 Homo sapi BC024233 Homo sapi M18415 Human plate AF262016 Homo sapi AX350512 Sequence AF281308 Homo sapi Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AC093116 F AC115398 F AC026346 F AB026898 F AX344975 AX348496 AL603644 BC004261 DNA AX350512 1350 bp Sequence 24 from Patent WO0179561. ALIGNMENTS ALL58163 AX350513 AF316894 MUSALP2ADB RRU79031 PIGA2AR SUMMARIES AF262016 HUMADRA2R AC113491 BTU79030 RATRG20 AC090342 AC114552 AP004085 AC105677 AB026898 AX344975 AX350512 AF281308 HUMADRA AY032736 AF284095 AX344974 AX348495 AE002058 AX348496 10 100 DB 100.0 1353 100.0 1521 100.0 3604 100.0 3612 100.0 3612 100.0 264908 96.1 1353 26621 39407 65069 64711 163156 127128 182224 188810 203230 1380 11378 1350 1353 1454 1552 1728 144494 Length 43147 126141 195076 204317 176291 163801 57.1 56.6 56.6 56.6 56.6 56.1 611.0 Query 57.1 57.1 57.1 57.1 100.0 AX350512 39.4 39.4 34.6 Score RESULT 1
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Result 8 8 טטט 00000

DNA polymerase III DNA polymerase III CDNA encoding mito

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1885.930 Million cell updates/sec
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                                                                                                              March 10, 2003, 18:24:01; Search time 48.9583 Seconds
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                              Compugen Ltd
           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compuc
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site, comprising; (b) detecting a polymorphic site comprising an alpha-2B, and alpha2A or alpha2C or fragment or complement of; and alpha-2B, alpha2A or alpha2C or guanine at positions 901-909 of (I), a site comprising oytosine or guanine at positions 901-909 or a site comprising (Vtosine or (B)) (ggggcggccg) or (B) (ggggcggctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, utility BHT933 and combinations of these) or arragonist (e.g. yohimbine, prazosin, ARC 239, reuwolscine, idazosan, tolazoline, phentolamine and combinations of these or predetermined response (where the response is correlated to adenylyl cycles. The companies of the physical compinations of compin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
                                                                                                                                                                                                           Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
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ive 0; Mismatches 0; Indels 0;
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/product= "alpha-2AAR"
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                 LIGGETT S B. SMALL K M.
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Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
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0
                                                                                                                                                                                                                                                                                                                                                                                                            96.1%; Score 39.4; DB 23; Length 1350; 97.6%; Pred. No. 0.00018; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     730 GGGGGCACCGAGGCCCAAGGTCTGGGCCCCGAGCG 770
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCCGAGCG 41
                                                                                                                                                                                           Disclosure; Page 152; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABQ47498 standard; DNA; 1733 BP
                                                           17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                            17-APR-2001; 2001WO-US12575
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                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                 Small KM;
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                                                                                                                                 WPI; 2001-611728/70.
                                                                                           LIGGETT S E
SMALL K M.
                                                                                                                                                                              a polymorphic site
                                                                                                                                         P-PSDB; AAM52123.
                WO200179561-A2.
                                                                                                                 Liggett SB,
                               25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ47498;
                                                                                           (LIGG/)
(SMAL/)
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ABQ47498
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Guetig

Berlin K,

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

01-SEP-2001; 2001WO-EP10074. 01-SEP-2000; 2000DE-1043826 05-SEP-2000; 2000DE-1044543.

WO200218632-A2.

07-MAR-2002

Homo sapiens.

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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylation then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligonucleotides and/or prognosis of side effects of the method is used: (i) for diagnosis and/or prognosis of side effects of the method is used: (i) for diagnosis and/or prognosis of side effects of the method is used: (i) for diagnosis and/or prognosis of side effects of the method is used: (i) for diagnosis and/or prognosis of side effects of the method polymorphisms (SNP's); and (ii) for differentiation of call or tissue polymorphisms (SNP's); and (ii) for differentiation of call or tissue methylation status of many C residues to be determinated simulaneously.

ARQ13410-ARQ54121 represent genomic DN sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                       gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
  drug; side effect; cancer; central nervous system; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 24; Length 1733; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990 GGGGGTATCGAGCGTAGGTTTAACGGTTTGGGTTTCGAGCG 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGCACCGAGCCCCAACGGTCTGGGCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                      Guetig D;
                                                                                                                                                                                                                                                                                                                                                      Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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ABQ47499 standard; DNA; 1733 BP
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75.6%;
                                                                                                                                                                                                                                             01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                        01-SEP-2001; 2001WO-EP10074
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Best Local Similarity 75.6
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-371829/40.
                                                                                                                       WO200218632-A2
                                                                                   Homo sapiens.
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methylation of a particular revealed in motif 5' CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic own that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the lasses of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the repeutic drugs and of a wide range of diseases, e.g. cancer, disorders the repeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ARQ1410-ARQ121 represent genomic DNA sequences used to illustrate the methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a novel method for determining the degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirthermatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 1733;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 GGGGGTATCGAGCGTAGGTTTAACGGTTTGGGTTTTCGAGCG 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGCACCGAGCCCAACGCTCTGGGCCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 25; DB 24
75.6%; Pred. No. 13;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL32072 standard; DNA; 7353 BP
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Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                WPI; 2002-371829/40.
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Berlin K;

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Piepenbrock C,
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(OZEN/)
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(BAUM/)
(TSEN/)
       olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAUS/)
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                                                                                                                                                                                                                                                                                                                                                           RESULT 7
AAZ94312/c
ID AAZ9431
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                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; defenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                         including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                   Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
                                                                                                                                                                                                                           Claim 1; SEQ ID NO 45; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGCACCGAGGCCCCAACGGTCTGGGCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human chemically treated genomic DNA #3.
                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD28362 standard; DNA; 7353 BP
                                                                                                                                                                                                                                                                                                                                                       61.0%;
75.6%;
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                                                                             02-JUL-2001; 2001WO-EP07537.
                                                                                                30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.6
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug abuse; migraine; ds
                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                         cytosine methylation
                                                                                                                                                                  WPI; 2002-130909/17
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                                        WO200200928-A2
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                      Homo sapiens
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                                                          03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                       Query Match
  gene; ds
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                                                                                                                                                                                                                                                                                                                                                                           Matches
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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonuclectides or peptide nucleic acid (PNA) oligoners useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder. Tourette's syndrom, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and sucidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                 Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein coupled receptor; cholecystokinin CCKB receptor;
rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baumbauch W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5730 ĠĠĠĠŦATĊĠĀĠĊĠŦĀĠĠŦŦŦĀĀĊĠĠŤŦŤĠĠĠŦŦŦĊĠĀĠĊĠ 5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat cholecystokinin CCKB receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birsan C,
                                                                                                                                                                                                                     Claim 1; Page 32-36; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silverman S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAI M.
SILVERMAN S.
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WPI; 2002-154759/20.
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Best Local Similarity
Matches 31; Conserv
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Kajkowski EM,
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This is the DNA sequence of a primer that was used in the PCR amplification of DNA encoding the N-terminal portion (including 22 amino acids proximal to the 5th transmembrane domain) of rat cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR). The PCR product was used in the construction of an intracellular loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion of IC3 of mammalian GPCRs is correlated with improved functional expression in yeast cells with retention of full ability to couple to the heterotrimeric G protein. The invention relates to mutant GPCRs with constitutively activating mutations that permit the activation of the receptors' functional activity in the absence of activating ligands, host cells that contain mutations that promote the functional activity of the GPCRs, host cells expressing such receptors, and vectors useful for making such cells. The host cells are useful in high throughput screening assays for therapeutic drugs, inserticides, mearacides etc., and are especially useful for assays.
                                 Novel host cells comprising heterologous G protein-coupled receptor modified to be constitutively active, useful for high throughput screening assays for e.g. drugs, insecticides or nematacides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New G protein-coupled receptors with a mutation in an intracellular domain, useful for high throughput screening assays for e.g. drugs, insecticides or nematocides
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alpha 2A adrenergic receptor; drug screening; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; Score 24; DB 21; Length 36; 100.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 BP; 2 A; 15 C; 16 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha 2A adrenergic receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%; Pred. No. 28;
Conservative 0; Mismatches
                                                                                                         Example 3; Page 25; 75pp; English
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 WPI; 2000-246753/21
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deputies of DNA encoding the N-terminal portion (including 3) amino acids proximal to the 5th transmembrane domain) of human alpha 2A adrenceptor, a G protein coupled receptor (GPCR). The PCR product was used in the construction of an intracellular loop 3 (IC3) deleted receptor mutant. Deletion of a portion of a mammalian GPCRs is correlated with improved functional expression in yeast cells with retention of full ability to cuple to the heterotrimeric G protein. The invention provides modified GPCRs having a mutation in IC3 that results in an improved functional response in cell-based assays. The modification promotes growth stimulation by a GPCR agonist, especially by improving coupling between the receptor and a heterotrimeric G protein. Polynucleotides encoding the mutated GPCR, chimeric G protein. Polynucleotides can be claimed. The modified GPCRs can be used in improved high recommendation by a GPCR agonist encoding the mutated GPCRs can be used in improved high chromomy structure screening assays (especially in yeast cells) for the content of the modified GPCRs can be used in improved high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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 This is the DNA sequence of a primer that was used in the PCR
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                                                                                                                                                                                                                                                                           throughput screening assays (especially in yeast therapeutic drugs, insecticides, nematacides etc.
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Best Local Similarity 100.(
Matches 24; Conservative
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30-JUN-2000;
07-JUL-2000;
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17-MAR-2000;
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19-MAY-2000;
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14-AUG-2000; 2000US-0225214.
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14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225268.
14-AUG-2000; 2000US-0225268.
14-AUG-2000; 2000US-0225268.
14-AUG-2000; 2000US-0225759.
14-AUG-2000; 2000US-0225759.
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14-AUG-2000; 2000US-0225759.
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14-AUG-2000; 2000US-0225759.
22-AUG-2000; 2000US-0225759.
23-AUG-2000; 2000US-0225759.
23-AUG-2000; 2000US-0225759.
23-AUG-2000; 2000US-0225759.
23-AUG-2000; 2000US-0229349.
01-SEP-2000; 2000US-0229349.
01-SEP-2000; 2000US-0229349.
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01-SEP-2000; 2000US-02293149.
06-SEP-2000; 2000US-02393149.
06-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
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2000US-0239935.
2000US-0239937.
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2000US-0232401.
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25-SEP-2000;
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21-SEP-2000;
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08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246612.
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08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
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2000US-0249265.
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2000US-0249218.
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Ruben SM

Rosen CA, Barash SC,

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 7495; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. Isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful on the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, harrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discreter e.g. Addison's disease, allergies, autoimmune characteristics, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discreter such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and copilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections.

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The present invention describes a polypeptide (I) which is a polymorphic variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase) ACAAl protein (BBB0516). ACAAl is located on chromosome 3p23-p22. (I) can be encoded by ABA91286 (or ABA91288) where the sequence comprises one of the haplotypes shown in Table 4 or one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are given in the specification. The polymucleotide encoding ACAAl can be used for providing haplotype and genotype information of an individual. Putthermore, the polymucleotide is useful for the treatment of disorders related to its abnormal expression or function. The present sequence represents the human ACAAl gene, featuring all the single nucleotide polymorphisms (SNP) possible, from the present invention.
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replace(14931,C)
                                                                                                 "single nucleotide polymorphism (SNP)"
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                                                        "single nucleotide polymorphism (SNP)"
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/standard_name= "single nucleotide polymorphism (SNP)'
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                                                     /standard_name=
replace(15471,C)
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replace(15486,G)
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les 30; Conservative
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DUDA A E.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                   Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22; peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype; single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "single nucleotide polymorphism (SNP)"
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replace(11756,C)
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replace(13390,T)
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                                                                                                                          Gaps
                                                                                         Score 23.4; DB 22; Length 14855;
Pred. No. 44;
0; Mismatches 11; Indels 0;
                                                         Sequence 14855 BP; 3335 A; 3554 C; 4013 G; 3953 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:1.
                                                                                                                                                                  265 GGCGGCTTCAAGGTGAGGCCCGAGGTCTGGGCGCCGAGTG 305
                                                                                                                                                1 GGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
replace(3546,A)
                                                                                                                                                                                                                                                  ABA93286 standard; DNA; 22028 BP
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replace(9182,A)
/*tag= h
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replace(14441,G)
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replace(4157,T)
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replace(4276,C)
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replace(9110,G)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace (4033,T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace (9600,G)
                                                                                         Query Match
Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
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/standard
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/standard
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Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22; peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype; single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide, comprising a polymorphic variant of the acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme thiolase) gene useful for providing haplotype information and in therapy for treating related disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.2%; Pred. No. 44;
Matches 30; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 22028 BP; 4808 A; 5592 C; 6133 G; 5476 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGGCACCGAGGCGCCCAACGGTCTGGGCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 85-93; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ47500 standard; DNA; 1733 BP
                                                                                                                                                                                                                                                           (GENA-) GENAISSANCE PHARM INC. (DUDA/) DUDA A E.
                                                                                                                                                                                                                           .8-MAY-2000; 2000US-205022P.
                                                                                                                                                                                     03-MAY-2001; 2001WO-US14330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard ambiguity codes.
                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-164134/21
                                                                                                                                                                                                                                                                                                                  Chew A, Koshy B;
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                                                                                                                 WO200187903-A2.
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                                                                               Homo sapiens
                                                                                                                                                     22-NOV-2001.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert convert convert convert convert convert convert converts the degree of but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. DNA that contains the target C is amplified acid (PNA) oligomers converts of oligomers and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers. The degree of methylation is calculated. The method cisused: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders contain nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide colymorphisms (SNP's); and (ii) for differentiation of call or tissue colymorphisms (SNP's); and (ii) for differentiation of call or tissue colymorphisms (SNP's); and (ii) for differentiation of call or tissue converts investigating call differentiation of call or tissue colymorphisms (SNP's); and (ii) for differentiation of call or tissue colymorphisms of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the contain and contains the degree of cytosine methylation described in
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of
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                                                                                                                                                                                                                                                                                                                   Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 CACCGAACGCAACCAACGATCTAAACCCCGAACG 704
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77.8%; Pred. No. 52;
:ive 0; Mismatches
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                                                    01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
              01-SEP-2001; 2001WO-EP10074.
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Matches 28, Conservative
                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                 (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                               WPI; 2002-371829/40.
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10-JAN-2002
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                                                                                                                                                                                                                                                   methylation of a particular cytosine in a motif 5'-0pG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclecides and/or peptide-nucleic acid [PNA] oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of call or tissue methylation status of many C residues to be determined simultaneously. ARQ13410-ARQ3412 represent genomic DNA sequences used to illustrate the chart of the contract of the degree of cytosine methylation described in
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                                                                                                                                                                                                                                        This invention describes a novel method for determining the degree of
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                         Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                               Guetig D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.2;
Pred. No. 52;
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XX
AC
ABL32073;
XX
AC
ABL32073;
XX
XX
ABL32073;
XX
XX
XX
Human immune system disease; cyton
XX
XX
XX
W
Human; immune system disease; cyton
XW
Antiarteriosclerotic; antianaemic;
XW
Antiarteriosclerotic; antianaemic;
XW
Antirheumatic; antiartric; antianaemic;
XW
Antirheumatic; antiartric; antianaemic;
XW
Antirheumatic; antiartricic; antianaemic;
XW
Antinflammatory; cancer; eye disease
XW
Acute myeloid leukaemia; Alzheimer
XW
YOURO200208-A2.
XX
PN
NO200200928-A2.
XX
PD
O3-JAN-2002.
XX
YX
PP
O2-JUL-2001; 2001WO-EP07537.
                                                                               Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.6%;
77.8%;
01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 28; Conservative
                                                                               Olek A, Piepenbrock C,
                                               (EPIG-) EPIGENOMICS AG.
                                                                                                           WPI; 2002-371829/40
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid thetkemia, Alzheimer's disease, Allo, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory(ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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Pred. No. 52;
0; Mismatches
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77.8%;
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30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.
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01-SEP-2000; 2000DE-1043826.
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Best Local Similarity 77.8'
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                                                                                                (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                               cytosine methylation
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Craim 1; Page 36-40; 190pp; English.

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The invention relates to nucleic acids comprising a segment of chemically createded DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonuclectides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behaviours, neurological disorders and cancer, in patricular major depressive disorder, routete's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, cd rung abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizopfrenic acid is useful for detecting the methylation schizophrenia. The nucleic acid is useful for detecting the methylation constant of all CpG dinucleotides and/or single nucleotide polymorphisms

XX

Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
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SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
Query Match
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0;
Oy 6 CACCAACGCCCAACGCCCAACGCGCAACGG 41

1619 CACCGAACGCAAACCCAACGATCTAAACCCCGAACG 1584

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Gaps

Search completed: March 10, 2003, 18:59:36 Job time : 56.9583 secs

Appli Appli Appli Appli Appli Appli Appl

Sequence Sequence

Sequence 1, P Sequence 1, P Sequence 1, P Sequence 31, P Sequence 49, Sequence 49, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 11, A

US-09-498-809-1 US-08-208-176-7 US-08-186-506-5 US-08-187-942C-31 US-08-188-228-49 US-08-312-643-43 US-08-312-638-49 US-08-312-638-49 US-08-312-638-49 US-08-317-942C-19 US-08-317-942C-1

JS-08-757-669A-19 JS-09-230-371A-19

ALIGNMENTS

```
APPLICANT: Takagi, Hiroshi
APPLICANT: Arafuka, Shino
APPLICANT: Marsui, Hiroshi
APPLICANT: Washizu, Kinya
APPLICANT: Washizu, Kinya
APPLICANT: Ando, Keiichi
APPLICANT: Roikeda, Sacoshi
TILLE OF INVENTION: Recombinant transglutaminase
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/77,447
FILING DATE: 19-07-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08136993; Patent No. 5420025; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-136-993-6
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75.0%;
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 27; Conservative
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ZIP: 20037-3202
FILING DATE:
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Sequence 12, Appli
Sequence 131, App
Sequence 1090, Ap
Sequence 1040, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 27, Appli
Sequence 3, Appli
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4352.932 Million cell updates/sec
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                                                                                                                          March 10, 2003, 18:31:11 ; Search time 2.88857 Seconds
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                                                                                                                                                                                                                                                1 gggggcaccgagcgcaggcc.....aacggtctgggccccgagcg
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-404-665-3
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Maximum Match 100%
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No.
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Gaps

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Score 21.6; DB Pred. No. 42; 0; Mismatches

DB 1; Length 225; Indels

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Query Match 52.7%; Score 21.6; DB 1; Length 1322; Best Local Similarity 75.0%; Pred. No. 41; Matches 27; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Cao, Hui
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT APPLICATION NUMBER: 60/066,517
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR PELING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131
LENGTH: 1436
                     NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STATE: Washington, D.C.
FITLE OF INVENTION: Recombinant transglutaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 decederresadedecedececeretrecedecede 317
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                                                                                                                                                                    COUNTRY: U.S.A.

ZIP: 20037-3202

COMPUTER READBALE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURSENT APPLICATION DATA:

APPLICATION NUMBER: US/08/136,993

FILING DATE:

APPLICATION NUMBER: US/08/136,993

FILING DATE:

APPLICATION NUMBER: US/08/136,993

FILING DATE:

APPLICATION NUMBER: US/07/77,447

FILING DATE:

APPLICATION NUMBER: US/07/77,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IMMEDIATE SOURCE:
; CLONE: pTV118 NcoI
US-08-136-993-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-199-637A-131
; Sequence 131, Application US/09199637A
; Patent No. 635841
; GENERAL INCRASSION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202.293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1322 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1322 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUNESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue CITY: N.W. STATE: Washington, D.C. COUNTRY: U.S.A. ZID.
                                                                                                                                                                                                                                                                                APPLICANT: Takagi, Hiroshi
APPLICANT: Takagi, Hiroshi
APPLICANT: Matsui, Hiroshi
APPLICANT: Mashizu, Hiroshi
APPLICANT: Ando, Keiichi
APPLICANT: Ando, Keiichi
APPLICANT: Noikeda, Satoshi
TITLE OF INVENTION: Recombinant transglutaminase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GGCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCC 224
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                                   1 GGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION DATE:
FILING DATE:
APPLICATION NUMBER: JP 2-282566
FILING DATE: 19-0CT-1990
TELEPHONE: 202-293-7060
TELEPHONE: 202-293-7060
TELEFAX: 202-293-7060
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/77,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/136,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08136993
Patent No. 5420025
                                                                                                                                                                                       US-08-136-993-8
Sequence 8, Application US/08136993
Patent No. 5420025
GENERAL INFORMATION:
APPLICANT: Takagi, Hiroshi
APPLICANT: Arafuka, Shino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takagi, Hiroshi
Arafuka, Shino
Matsui, Hiroshi
Washizu, Kinya
Ando, Kelichi
Koikeda, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Takagi,
APPLICANT: ATCHUKA,
APPLICANT: MATSHI,
APPLICANT: WASHIZU,
APPLICANT: ANGO, Kei
APPLICANT: KOIKeda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-136-993-12
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US-08-998-416-1040
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                                                                                                                         Gaps
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                                                                          Query Match 52.2%; Score 21.4; DB 4; Length 1436; Best Local Similarity 80.6%; Pred. No. 47; Matches 25; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 1; Length 1123;
Pred. No. 64;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GÉCTTGGAGGCCTGGCCCACCAGTCTGGGTCGCGAGC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,626
FILING DATE: Filed Herewith
ATTORNEY/AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0115 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION DATA OF THE TELEPHONE: A15-855-0555
                                                                                                                                                                                                 1187 GGGCGCCGAGCCAGCAACCGCCTGGGC 1217
                                                                                                                                                           3 GGGCACCGAGCGCAGGCCCAACGGTCTGGGC 33
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Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08700626
Patent No. 5734038
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX.

TELEFAX.

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Innear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: PGANNOTOI
CLONE: 620984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 27; Conserva
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.
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                                                                                                                                                                                                                                                               RESULT 5
US-08-700-626-2/c
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Gaps
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Steiner, Sabine
Mohr, Christine
Mohr, Orbitatine
Knechtle, Philipp
Rebischung, Cotinne
VRENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr. Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION DATA:

APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.7%; Score 20.8; DB 4; 1
Best Local Similarity 70.0%; Pred. No. 75;
Matches 28; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 GGCAGCACCGACGCCTGGCCCAACAGGCTCGACAGCGAGC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGCACCGAGGCCCAACGGTCTGGGCCCCGAGC 40
                                                                                                                                                                                                                            ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 623926dartis Corporation
SEET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1040, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1664UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 598 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                              APPLICANT: Wendland, Jun
APPLICANT: Knechtle, Phi
APPLICANT: Rebischung, C
TITLE OF INVENTION: GENC
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDESS:
ADDRESSEE: No. 6239264
                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
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LOCATION: 24090..25177.

DENTIFICATION METHOD: experimental
DENTIFICATION FORMATION: (Lanction= "(translation start:
OTHER INFORMATION: 24110;"
OTHER INFORMATION: Avidence= Experimental
OTHER INFORMATION: /Gene= "ACHE"
OTHER INFORMATION: /Gene= "ACHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: promoter COCATION: 4089..22464 OCCATION: 4089..22464 OCHER INFORMATION: /buction= "ACHE Promotor" OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: exon
LOCATION: 22465..2537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRATURE:
NAME/KEY: exon
LOCATION: 25524. 26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 4
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/gene= "ACHE"
/number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMI
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    experimental
                      TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: exon
LOCATION: 27255..28007
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tocation: 28008..28129
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OTHER INFORMATION: /evi
OTHER INFORMATION: /ger
OTHER INFORMATION: /mun
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27385..27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    terminator
28129..28131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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Fatent No. 6025183

GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Salut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                COUNTRY: NO. CLASSING STATES OF THE STATES O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 GGCAGCACCGACGCCTGGCCCAACAGGCTCGACAGCGAGC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.7%; Score 20.8; DE Best Local Similarity 70.0%; Pred. No. 75; Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
RESISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
      STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: PAG1635UP
US-08-998-416-1040
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SEQ ID NO:25:
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LOCATION: complement (34528..34895)
OTHER INFORMATION: function= "arsenite resistance OTHER INFORMATION: gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
SEATURE:
NAME/KEY: exon
                                                                                                                                                            LOCATION: COMPLEMENT (34092..34358)
OTHER INFORMATION: / Gene= "AR"
OTHER INFORMATION: / Gene= "AR"
OTHER INFORMATION: / Gene= "AR"
LOCATION: Complement (3379..33963)
OTHER INFORMATION: / Gene= "AR"
OTHER INFORMATION: / Gene= "AR"
OTHER INFORMATION: / Mumber= 3
FEATURE:
NAME/KEY: exon
OTHER INFORMATION: / Gene= "AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
FEATURE:
NAME/KEY: exon
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
FEATURE:
NAME/KEY: exon
LOCATION: complement (31131..31284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
PEATURE: /number= 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: exon
LOCATION: compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
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49.8%; Score 20.4; DB 6; Length 294;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

49.8%; Score 20.4; DB 6; Length 232;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
531889-25/C
; Patent No. 5318899
; RAPLICANT: SCARBOROUGH, ROBERT M.; WOLF, DAVID L.; CHARO,
; ISRAEL F.
; TILLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; TUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-COT-1989
; APPLICATION NUMBER: 367,809
; PRING DATE: 16-JUN-1989
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
5318899-27/c
;Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ISRAEL F. | INTERVION: PLATELET AGGREGATION INHIBITORS |
| TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS |
| NUMBER OF SEQUENCES: 83 |
| CURRENT APPLICATION DATA: |
| APPLICATION NUMBER: US/07/483,229 |
| FILING DATE: 20-FEB-1990 |
| APPLICATION NUMBER: 418,028 |
| FILING DATE: 06-OCT-1989 |
| APPLICATION NUMBER: 36',509 |
| FILING DATE: 16-JUN-1989 |
| SEQ ID NO:27: |
| LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 GGCACTGATCACAGCACAGACCGTCTGCGCACTGAGCG 149
                                                                                                                                                                                                                                                                                                                                                                                                            Db 22583 GGGCACCGTGCGTCCCCGAGGGTCCAGGCCCC 22617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GGCACTGATCACAGCACAGACCGTCTGCGCACTGAGCG 87
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                                                                                                                                                                                                                                                                                                                                                                             2 GGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCC 36
                                                                                                                                                                                                                                                                     Query Match
50.2%; Score 20.6; D
Best Local Similarity 74.3%; Pred. No. 79;
Matches 26; Conservative 0; Mismatches
LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
FEATURE:
NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
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KESULT 13
US-08-923-454A-17/C
Sequence 17, Application US/08923454A
Sequence 17, Application US/08923454A
Sequence 17, Application US/08923454A
Sequence 17, Application US/08923454A
Septence 17, Application US/08923454A
SAPLICANT: Livi, George
APPLICANT: Livi, George
APPLICANT: Clinkenderd, Helen
APPLICANT: Suran, Eric
STREET: 709 Swedeland Road
CITY: King of Prussia
STREET: PA
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 2651 édéchécécegéchadcacardardeherredececeahec 2614
3 GGGCACCGAGGCCCCAACGGTCTGGGCCCCGAGC 40
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Pred. No. 95;
0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-977-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 9934 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 612-332-53
TELEFAX: 612-332-9081
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Patent No. 6232112

GENERAL INFORMATION:

APPLICANT CATCHESIDE, DAVID E.

TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION

TITLE OF INVENTION: OF DNA

TYTLE OF INVENTION

T
                                                                                                                                                                      Sequence 1, Application US/08977171
; Sequence 1, Application US/08977171
; Patent No. 622212
; GENERAL INFORMATION:
TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6232112west Center, 90 South 7th Street
STATE: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,171
CLASSIFICATION DATA:
PRICATION NUMBER:
APPLICATION DATA:
APPLICATION DATA:
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Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10552.130801
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ATORNEY/AGENT INFORMATION:
NAME: SKOGG, MARK TREGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 1055:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEPAX: 612-332-59081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-977-171-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 9775 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
                                                                                                                   RESULT 11
US-08-977-171-1/c
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US-08-977-171-2/c
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Gaps
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Length 9934;
                                Indels
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REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
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Gaps

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Query Match 48.3%; Score 19.8; DB 1; Length 51; Best Local Similarity 69.2%; Pred. No. 1.7e+02; Matches 27; Conservative 0; Mismatches 12; Indels
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US-07-60-93D-27

Sequence 27, Application US/0769093D

Patent No. 540386

GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWART, Andrew G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUGHRARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 25-UNN-1991
CLASSIFICATION NUMBER: US/07/690,983D
FILING DATE: 24-AUN-1991
CLASSIFICATION NUMBER: 199768

REGISTRATION NUMBER: 199768

REGISTRATION NUMBER: 16786/148 CHAC
TELEPHONE: (202)672-5399
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LEMPTH: ADDRICACED CACH
SELEPA: (202)672-5399
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LEMSTH: STANDENDES: double
TTELEPHONE: CACHOLICACH
TYPE: nucleic acid
STRANDENDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature;
10.CATION: 13..42
OTHER INFORMATION: /note= "Coding sequence for LHRH
US-07-690-983D-27
                                                                                        /note= "Coding sequence for LHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCCGAGCG 41
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                                                                                                                                 analogue'
    NAME/KEY: misc_feature
LOCATION: 13..42
OTHER INFORMATION: /not
OTHER INFORMATION: ana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                              1..51
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CLONE: DBTA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..54
                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 1..!
US-07-690-983D-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FOUNDER.

CITY: Washington, D.C.
CUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FLING DATE: 25-JUN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/AU90/00373
FLING DATE: 24-AUG-1990
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CHAC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGCACCGAGCCCAACGCTCTGGCCCCGAGCG 41
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
HYPOTHETICAL: Feature polymorphism at 1325
US-08-923-454A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/07690983D
Patent No. 5403586
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J.
APPLICANT: TSONIS, Con G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA IMMEDIATE SOURCE: FEATURE: PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INPORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 51 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPLOGY: linear MOLECHTE
                                                                                                                                                 INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-690-983D-17
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                             0; Gaps
Query Match 48.3%; Score 19.8; DB 1; Length 54; Best Local Similarity 69.2%; Pred. No. 1.7e+02; Matches 27; Conservative 0; Mismatches 12; Indels
                                                        Search completed: March 11, 2003, 07:41:04 Job time : 20.8886 secs
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Sequence 3, Application US/10124429
Publication No. US20020187525A1
GENERAL INFORMATION:
APPLICANT: TAGUCHI, SEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
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                                                                                                                                                                               (without alignments)
620.211 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               March 11, 2003, 00:54:30 ; Search time 44.1538 Seconds
                                                                                                                                                                                                                                                                                                         1 gggggcaccgagcgcaggcc.....aacggtctgggccccgagcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/prodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/prodata/2/pubpna/DCT NEW PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/USO6_NEW PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/USO6_NEW PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/USO7_NEW PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/USO8_NEW PUB.seq:*

7: /cgn2_6/prodata/2/pubpna/USO8_NEW PUB.seq:*

8: /cgn2_6/prodata/2/pubpna/USO8_NEW PUB.seq:*

9: /cgn2_6/prodata/2/pubpna/USO8_NEW PUB.seq:*

10: /cgn2_6/prodata/2/pubpna/USO8_NEW PUB.seq:*

11: /cgn2_6/prodata/2/pubpna/USO9_NEW PUB.seq:*

12: /cgn2_6/prodata/2/pubpna/USO9_NEW PUB.seq:*

13: /cgn2_6/prodata/2/pubpna/USO9_NEW PUB.seq:*

14: /cgn2_6/prodata/2/pubpna/USO9_PUBCOMB.seq:*

15: /cgn2_6/prodata/2/pubpna/USO9_PUBCOMB.seq:*

16: /cgn2_6/prodata/2/pubpna/USO9_PUBCOMB.seq:*

17: /cgn2_6/prodata/2/pubpna/USO9_PUBCOMB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-975-719-131

US-09-865-50-1483

US-09-865-50-1483

US-09-865-50-1483

US-09-864-761-536

US-09-864-761-536

US-09-805-467A-3

US-09-805-467A-3

US-09-805-467A-3

US-09-805-467A-3

US-09-819-104A-3

US-09-913-86-8800

US-09-923-876-2800

US-09-923-876-1884-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                   478924 seqs, 333959956 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match
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Sequence 4927, Application US/09983965

Sequence 4927, Application US/09983965

Sequence 4927, Application US/09983965

Sequence 4927, Application US/09983965

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: WHORER: US/09/983,965

CURRENT FILING DATE: 1909-12-15

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 5912
  Sequence 1, Appli
Sequence 3, Appli
Sequence 3102, Ap
Sequence 2102, Appl
Sequence 25, Appl
Sequence 2208, Appl
Sequence 208, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
                                                                                                                                          Sequence 11, Appl
Sequence 9, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 17, Appli
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21, Appl
19, Appl
23, Appl
4, Appli
1, Appli
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Sequence 23,
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0 US-09-751-962-1

0 US-09-751-962-2

0 US-09-960-352-3868

0 US-09-864-761-9102

0 US-10-037-806-25

0 US-10-034-623-25

0 US-10-027-806-2

0 US-09-764-867-1018

0 US-09-764-860-1018

0 US-09-796-88-37

0 US-09-796-88-37

0 US-09-796-88-37

0 US-09-938-330-13

0 US-09-938-330-13

0 US-09-938-330-13

0 US-09-938-330-17

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0 US-09-938-330-17

0 US-09-938-330-17

0 US-09-938-330-13

0 US-09-938-370-13

0 US-09-938-3768

0 US-09-938-3768

0 US-09-938-3768
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US-09-983-965-4927
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ilarity 74.4%; Pred. No. 15;
Conservative 0; Mismatches 10.
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 99775
9934
440
555
837
837
18385
42432
3471
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Best Local Similarity
....hes 29; Conserve
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TYPE: DNA
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APPLICANT: MOMOSE, HARUO
TITLE OF INVENTION: A METHOD OF PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REFERENCE: 220567USOCONT
CURRENT APPLICATION NUMBER: US/10/124,429
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: PCT/JP00/07135
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 3
LENGTH: 1809
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Patent No. US20020132753A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTATON NUMBER: US/09/764,864
CURRENT APPLICANT NUMBER: US/09/764,864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICANT: Rabme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE REFERENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT PELLING DATE: 1998-11-25
PRIOR PILLING DATE: 1998-11-25
PRIOR PELLING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FASTERE (FOR Windows Version 4.0
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80.6%; Pred. No. 52;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 27; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.6
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (578)..(1798)
; OTHER INFORMATION:
US-10-124-429-3
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                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Conduley, Pamela
APPLICANT: Conduley, Pamela
APPLICANT: Conduley, Pamela
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and I
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09/867,550
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SEQ ID NO 14437
SEQ ID NO 14437
LENGTH: 569
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0
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 389 LENGTH: 514
                                                                                                                                                                                       Length 514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
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Pred. No. 71;
0; Mismatches 10,
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Pred. No. 71;
0; Mismatches 10;
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Patent No. US20020082206A1
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Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-859-101-2/c
; Sequence 2, Application US/09859101
; Sequence 2, Application US/09859101
; Setent No. US20020068825A1
; GENERAL INFORMATION:
                                                                                                                                                                                             51.2%;
73.0%;
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73.0%;
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COMPUTER READABLE FORM:
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Best Local Similarity 73.0°
                                                                                                                                                                                                                                    Conservative
                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-864-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-09-867-550-1483
                                                                                                                                                                                                             Best_Local Similarity
Matches 27; Conserva
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ORGANISM: Homo sapiens
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SEQ ID NO 5736
LENGTH: 457
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APPLICANT: Wehrman, Tom
APPLICANT: Olan, Klachong B.
APPLICANT: Olan, Klachong B.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
CURRENT FAPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: pt_Lgenes Version 1.0
SEQ ID NO 134-
LENGTH: 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.2%; Score 21; DB 10; Length 1123; Best Local Similarity 73.0%; Pred. No. 71; Matches 27; Conservative 0; Mismatches 10; Indels
                                        CURRENT AFFICATION DAIAN
CURRENT AFFICATION NUMBER: US/09/859,101
FILING DATE: 14-May-2001
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: US/08/700,626
FILING DATE: «Unknown»
ATTORNEY/AGENT INCORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0115 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 255-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
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; CLONE: 620984
; SEQUENCE DESCRIPTION: SEQ 1D NO: 2:
US-09-859-101-2
  SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 134, Application US/10098841 Publication No. US20020197679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Xo, Chonglun APPLICANT: Xo, Chonglun APPLICANT: May, Yunqing APPLICANT: Mang, Jan-Rui APPLICANT: Ren, Feiyan APPLICANT: Ren, Feiyan APPLICANT: Wang, Dunrui APPLICANT: Wang, Dunrui APPLICANT: Wang, Dunrui APPLICANT: Wang, Ziwei APPLICANT: Wang, Ziwei APPLICANT: Wang, Zhiwei APPLICANT: Wang, Zhiwei APPLICANT: Weirman, Tom APPLICANT: Weirman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-098-841-134/c
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Gaps
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APPLICANT: Chen, J. Don

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: UNG-030

CURRENT PILLON NUMBER: US/09/819,104A

CURRENT PILLON DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/193,138

PRIOR APPLICATION NUMBER: 60/193,138

PRIOR FILING DATE: 2000-03-29

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 3

LENGTH: 7521

TYPE: DAA

ORGANISM: Homo sapiens

FEATURE:

NAMEKEY: CDS

1000-03-03

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1300-03-03

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1500-03-03

1600-03-03

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Sequence 1, Application US/09819104A

Publication No. US2030027137A1

GENERAL INFORMATION NO. US2030027137A1

APPLICANT: Chen, J. Don

TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: UMG-030

CURRENT APPLICATION NUMBER: US/09/819,104A

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 6

SOUTH NOS: 6

SOUTH NOS: 10 NOS: 6

SEQ ID NO 1

LENGTH: 8686
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                                             1 GGGGGCACCGAGCCCAACGGTCTGGGCCCCCGAGC 40
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; Pred. No. 84;
0; Mismatches
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                                                                                                                                                                                                                                                            Sequence 3, Application US/09819104A Publication No. US20030027137A1
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Matches 28; Conservative
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Best Local Similarity 70.0
Matches 28; Conservative
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; LOCATION: (157)..(7677)
US-09-819-104A-1
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                                                                                                                                                                                                 RESULT 11
US-09-819-104A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-819-104A-3
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 3.2
US-09-864-761-5736
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; Sequence 1, Application US/10006950
; Patent No. US20020161216A1
; GENERAL INFORMATION:
APPLICANT: Bonini, James A.
TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF4 RECEPTOR
FILE REFERENCE: 58799
; CURRENT APPLICATION NUMBER: US/10/006,950
; CURRENT APPLICATION NUMBER: US/10/006,950
; PRIOR APPLICATION NUMBER: US/10/006,950
; PRIOR PILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver: 2.0 - beta
; SEQ ID NO.
; LENGTH: 1461
                                                                                                                                                                                                                                                                                                                          Score 20.8; DB 10; Length
Pred. No. 82;
0; Mismatches 12; Indels
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Patent No. US20020058259A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human Lipoxin A4
TITLE OF INVENTION: Receptor-Like Protein
FILE REFERENCE: 4974.00453
CURRENT PELLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 06/189,037
PRIOR APPLICATION WHORE: 60/189,037
PRIOR SEQ ID NOS: 5
SOFTWARE: FASELSEQ for Windows Version 4.0
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Best Local Similarity 70.0%;
Matches 28; Conservative
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Best Local Similarity 70.0
Matches 28; Conservative
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US-10-006-950-1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 28; Conser
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LENGTH: 2300
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US-09-805-467A-3
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OTHER INFORMATION: n equals a,t,g,
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Sequence 4787, Application US/09783590

Parent No. US20020110850A1

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haddong
APPLICANT: Li, Haddong
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genee, Sequences, and Expression Products 16.2
CURRENT APPLICATION WUMBER: US/09/783,590

CURRENT APPLICATION NUMBER: US/09/783,590

CURRENT APPLICATION NUMBER: 08/420,856

PRIOR APPLICATION NUMBER: 08/420,856

PRIOR APPLICATION NUMBER: 08/420,856

PRIOR PILING DATE: 1994-11-21

PRIOR FILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485

SOGTWARE: PatentIn Ver. 2.0

SEQ ID NO 4787
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              Sequence 216, Application US/09764860

Patent No. US20020094953A1

GENERAL INFORMATION:

APPLICANT ROSEN et al.

TITLE OF INVENTION:

CURRENT APPLICANTION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper;

NUMBER OF SEQ ID NOS: 1198

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 216

LENGTH: 239
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Best Local Similarity 74.3%; Pred. No. 96;
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (213)
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US-09-764-860-216
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OTHER INFORMATION: human genomic region containing ltrpc5
OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1
OTHER INFORMATION: containing KvLQT1 gene)
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Sequence 6, Application US/10026188

Patent No. US20020164645A1

GENERAL INFORMATION:

APPLICANT: Zhang, Yifeng

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Assays for Taste Receptor Cell Specific

TITLE OF INVENTION: Assays for Taste Receptor Cell Specific

TITLE OF INVENTION: Lon Channel

FILE REFERENCE: 02307E-114910US

CURRENT APPLICATION NUMBER: US/10/026,188

CURRENT PILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: US 60/259,379

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 6

SEQ ID NO 6

FERNANCE: PRESENCE OF Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 366;
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US-09-783-590-4787
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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LOCATION: (246)
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NAME/KEY: misc feature
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ORGANISM: Homo sapiens
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US-10-026-188-6
Query Match 50.2%; Score 20.6; DB 9; Leng
Rest Local Similarity 74.3%; Pred. No. 1e+02:
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Search completed: March 11, 2003, 23:15:29 Job time : 79.1538 secs

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AL606540 Chicken a BM35281 1969h02.y AL530418 AL530418 BQ887729 AGENCOURT BQ302172 QVO-BT026 BQ923710 AGENCOURT

AL236849 Terracdon AL256895 Terracdon AL2544577 AL544577 AL237702 Terracdon BE64878 UI M-BH2. AL606561 Lamprey a AL606541 Chicken a AL234292 Terracdon BIS679 601089610 AL234292 Terracdon AL606559 Herring a AL606568 Sea Horse AL60656 Toothcarp AL60656 Roa Horse AL60656 Horse alph AL60656 Horse alph AL60656 Chorse alph AL606576 Sturgeon AL506574 Sturgeon AL506574 Sturgeon AL506574 Sturgeon AL606574 Sturgeon AL606574 Sturgeon

Scoring table:

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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaeetner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillet, L., Martan, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ij32d04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMPN 11near EST 29-APR-2002 ij32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA clone IMAGE:6136374 5' similar to SW:AZAA_HUMAN P08913 BM967248
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
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AKO18378
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SCAAZCAR
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JOURNAL
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BM967243 ij32c09.y
BB643669 BB643669
BQ129312 ij34d05.y
BI453981 603200147
BI838282 603083213
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                  GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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    Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this

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                  Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
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                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="ImAGE:6136374"
/clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
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100.0%; Pred. No. 2.8e-92;
live 0; Mismatches 0; Indels (
                                                                                  (brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seg primer: -40RP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
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/dev stage="Adult"
/lab_host="DH108"
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                                                                                                                                                                                                                       organism="Homo sapiens"
  Email: dmelton@biohp.harvard.edu
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/noce="Organ: Pancreas; Vector: pSPORTI; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using Superscript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on Solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; O.S microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library.
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1 (bases 1 to 492)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theisling, B., Ritter, B., Ronko, I., Bennett, J., Cardenas, M., Globons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Endocrine Pancreas Consortium
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing dassington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
(brown@fas.harvard.edu)
Sossible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.
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1j32c09.v1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136336 5' similar to SW:AZAA_HUMAN P08913
ALPHA-2A ADRENBEGIC RECEPTOR ;, mRNA sequence.
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| Organism="Homo sapiens"
| /organism="texon:9606"
| /clone="IMAGE:6136336"
| /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
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Other_ESTs: ij32c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
GGGCGCCAGAACCGCGAGAAGCGCTTCACGTTCGTGCTGGCCGTGGTCATCGGAGTGTTC
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/dev_stage="Adult"
/lab_host="DH10B"
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1 (bases 1 to 691)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Cokazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takedai, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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                                                                                679 ACCCGCGTGCCACCCAGCCGCGGGGTCCGGACGCCGTCGCCGCCGCCGCGGGGGGGCACC
                                                                                                                                                                                       252 GGCCCCCCAGACCCGAGCGCGGTCCCCGGGGCAAAGGCCCGAGCCCGAGCCCAGGTG
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  DB 14; Length 492;
                                        Indels
                     Pred. No. 1.8e-79;
0; Mismatches 1
36.3%; Score 490.4;
99.8%; Pred. No. 1.80
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                     Best Local Similarity
Matches 491; Conservative
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KEYWORDS
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Full further details.
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/clone="B2303352011"
/clone_lib="RIKEN full-length enriched, adult male corpora
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/dev stage="adult"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. let strand cDNA was CAGAGAAGCATCCAAGAGCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
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/ Lissue type="Islets of Langerhans"
/ dev_stage="Adult"
/ lab_host="DAULt"
/ lab_rote="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
/ Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). CDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms POR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.1e-72;
iive 0; Mismatches 0;
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NIH-MGC http://mgc.nci.nih.gov/.
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E (Bases 1 to 453)

E (Bases 1 to 453)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTS: ij3405.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 bp mRNA linear EST 29-APR-2002 ij3405.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA clone IMAGE:6136736 5' similar to SW:AZAA_HUMAN P08913 BQ129312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6136736"
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Fax: 617-495-8557
Email: dmelton@biobp.harvard.edu
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RESULT 4 BQ129312/c LOCUS DEFINITION

ORGANISM

AUTHORS REFERENCE

VERSION KEYWORDS SOURCE ACCESSION

TITLE JOURNAL COMMENT

source

FEATURES

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/db xref="taxon:9666"
/clone=InAGE:226634"
/clone=Inb="NIH MGC_97"
/lab_host="DH10B"
/nore="Organ: testis, Vector: pBluescriptk (modified force="Organ: testis," Site 1: BamH1; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH1; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad pBluescript KS+); Site 1: BamH2; Site 2: Sall-xhoI (grogad primer size 2: Sk and normalized to ROT 5: This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                      Unpublished (1999)

Conteat: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1671 row: m column: 11

High quality sequence stop: 716.
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30.4%; Score 410.6; DB 13; Length
Best Local Similarity 86.0%; Pred. No. 6.1e-65;
Matches 586; Conservative 0; Mismatches 74; Indels
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NIT-MGC http://mgc.nci.nih.gov/.

NIT-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

CLONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Liminge.llnl.gov

Plate: LLAMILSS row; i column: 04

High quality sequence stop: 740.

Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)
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                                                                                                                     584 GGTACGTCATCTCGTCGTG---CATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCC
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4e-62;
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100.0%; Pred. No. ...
... 0; Mismatches
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GGAA2AAR
Chicken alpha2 adrenergic receptor gene fragment probably subtype
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Gallus gallus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves; Neognathae, Galliformes; Phasianidae,
Phasianinae, Gallus.
1 (bases 1 to 855)
Hunter,C. and Elgar,G.
Alpha2 adrenergic receptor gene
1 (hases 1 to 655)
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Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmp.mrc.ac.uk
Location/Qualifiers
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480 CGGGCGCT-GCGCCGCCACAGAACCTCTTCCTGGTGTCGCTGGCCTCGGCCGACATCCTG
                                                                                                                  424 AACCTGAAGCGCACGCCGCGCATCAAGGCCATCATCATCACCGT-GTGGGTCATCTC
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65.8%; Pred. No. 1.6e-48;
ive 0; Mismatches 223;
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GSS; Alpha2 adrenergic receptor gene.
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/db_xref="taxon:9031"
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/db_xref="taxon:9606"
/clone="csollo121yC24"
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/clone="csollo121yC24"
/clone="type="placenta"
/clone lib="LTI NFL06 PL2"
/clone="type="placenta"
/note="vector: pCWNSPORT 6; Site l: Not!; lst strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: filangchifetech.com URL: http://fullength.invitrogen.com" 3 others
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Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1077)
1 (bases 1 to 1077)
1 (Aruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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           121 CGTCGCGCTGGCGCGGGCGGCAGAACCGCGAGAAGCGCTTCACGTTCGTGCTGGCCGTGG 180
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 rearcedagrerregrerecrecrecrecrecrerrerrerreactacedecreaced
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75.1%;
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a ò 엄 Melton, D., Brow, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Taagareishvili, R., Williams, T., Dackson, Y. and Bowers, Y.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 358)

sapiens

ORGANISM

SOURCE

Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu

Unpublished (2000)
Other\_ESTs: ig69h02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wstl.edu)

Possible reversed clone: similarity on wrong strand Seg primer: -40RP from Gibco High quality sequence stop: 342. Location/Qualifiers

source

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REFERENCE
AUTHORS
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286 ATGGGCTACTGGTACTTCGGCAAGGCTTGGTGCGAGATCTACCTGGCGCTCGACGTGCTC
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                                                                                                                                                                              ACCGTGTGGGGTCATCTCGGCCGTCATCTCCTTCCCGCCGCTCATCTCCATCGAGAAGAAG
                                                                                                                                                                                                  181 ATGTCTGGGTCATCTCGGCCGTCATCTCCTTCCGCCGCTCATCTCCATAGAGAAG
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                                                         TICTGCACGICGACCATCGTGCACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATC
                                                                                                                    ACACAGGCCATCGAGTACAACCTGAAGCGCACGCCGCGCCGCCATCAAGGCCATCATCATC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HR85 islet"
/tlssue_type="Purified pancreatic islet"
/tlssue_type="Purified pancreas"
/tlssue_type=
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1969h02.yl HR85 islet Homo sapiens CDNA 5' similar to SW:A2AA_HUMAN P08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
BM352981
BM352981.1 GI:18085339
EST.
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1325

DEFINITION

ACCESSION VERSION KEYWORDS

59

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is a NIH MGC Library.
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BQ887729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: brain, Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end carriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Forg Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8131 Email: filang@lifetech.com URL: http://fullength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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ALS30418 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD007YE02 5
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens between the between the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 CATCGCCGTGTTCACGAGCCGCGCGCTCAAGGCGCCCCAAAACCTCTTCCTGGTGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 GATCGCCCTTCTGACCAGCCGGCGCT-GCGCCCCCCACAAAACCTCTTCCTGGTGTCGCT
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="cSODD007XE02"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                                                                                                                                                                                                                      AL530418.1 GI:12793911
                               58 TCGGGGGGACAGGAAGCGGAT 38
                                                                                                                                                                                                                                    prime, mRNA sequence.
407; Conservative
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/db xref="taxon:10090"
/clone="IMAGE:6313133"
/clone=lba:"MAGE:6313133"
/clone=lba:"MH MGC 129"
/lab-host="DH10E (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
pcMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2. Xb: Constructed by ResGen, Invitrogen Corp. Note: this
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AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 297)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., ad Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.F., Nagai, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M., Saia, J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BT0263-101299-072-h10&t3=1999-12-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 205.
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/db xref="taxon:9606"
/db xref=staxon:96053"
/dev stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
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QVO-BT0263-101299-072-h10 BT0263 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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CTGCACGTCGTCCATCGTGCACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATCAC
                                 CGTGTGGGTCATCTCGGCGTCATCTCCCGCCGCTCATCTCCATCGAGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                       379 CGACGCCCC-----GCCTATCCGCAGTGCGGCCTCAACGATGAGACCTGGTA
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                                                                                                               ACAGGCCATCGAGTACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 CGTGCGCATCTACCAGATCGCCAAGCGTCGCACCCGCGTGCCACCCAGCCGCCGGGGTCC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 935)

1 (Dases 1 to 935)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MCC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://mage.llnl.gov

Plate: LLAM13611 row: b column: 15

High quality sequence stop: 535.

10.935
Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 7.76 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            935 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8803211 Lupski_sciatic_nerve Homo sapiens cDNA clone
EQ923710
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                          DB 14; Length 297;
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/db_xref="taxon:9606"
/clone="IMAGE:6198830"
/clone lib="Lupski_sciatic_nerve"
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DB 17; Length 896;

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others

617

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797 441

us-09-636-259c-1.rst

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CNSO2NV2 966 bp DNA linear GSS 14-MAY-2000 Terraodon nigroviridis genome survey sequence T7 end of clone 152E12 of library G from Tetraodon nigroviridis, genomic survey
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Tetradon nigroviridis.

Tetradon nigroviridis.

Tetradon nigroviridis.

Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata, Teleostei; Neoteleostei;

Acainopterygii; Teleostei; Buteleostei; Neoteleostei;

Reanthomorpha; Acanthopterygii; Percomorpha; Tetraddontiformes;

Tetradontidae; Tetradon.

1 (bases 1 to 966)

Boses-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Mincker, P., Brottier, P., Quetier, F.,

Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                          GIGITCGGCAACGIGCICGICATCATCGCGTGTTCACGAGCCGCGCGCGCTCAAGGCCGCCC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAAACCTCTTCCTGGTGTCTCTGGCCTCGGCCGACATCCTGGTGGCCACGCTCGTCATC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTITICICGCIGGCCAACGAGGICAIGGGCTACTGGIACTICGGCAAGGCTIGGIGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 ATCIACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCCTGTGCACCTGTGCGCCATC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTTGGACCGCTACTGGTCTGTCACGCAGGCGGTCCAGTACAACCTGAAGAGGACCCCT 857
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Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="012P03"
/clone_lib="G"
/note="Genoscope sequence ID : COBK
PUC-Ori"
                                                                                                                                                                                                                                          Score 226.4; DB 17
Pred. No. 1.7e-31;
1; Mismatches 92
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AL205895.1 GI:7864714
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Best Local Similarity 75.1%;
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS03BQW 896 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 012P03 of library G from Tetraodon nigroviridis, genomic survey
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCG-3' and
5'-GACTAGTTCTAGATCGCGACCGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                            2
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostoni,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetraodontidae, Tetraodon.

I (bases, 1 to 896)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene number estimate provided by genome wide analysis using Terraodon nigrovixidis DNA sequence Unpublished
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Rosel-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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Pred. No. 1e-36;
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Tetraodon nigroviridis.
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Fisher, C.,

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2E 3 (bases 1 to 966)

"RS Genoscope.

Juncet Submission

NAL Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.

DES Location/Qualifiers

Source Abbaref="texon:99883"

Abbaref="texon:99883"

Aclone="152B12"

Aclone="152B12"

Anote="Genoscope sequence ID: COAGI52BCO6LP1~end: T7"

Anote="Genoscope sequence ID: COAGI52BCO6LP1~end: T7"
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Best Local Similarity 75.5%; Pred. No. 2.4e-29;
Matches 265; Conservative 1; Mismatches 85; Indels 0;
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## GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic

March 11, 2003, 00:54:30 ; Search time 1453.85 Seconds (without alignments) 620.211 Million cell updates/sec Run on:

Title: Perfect score:

US-09-636-259C-1 1350 1 atgggctccctgcagccgga......gggacaggaagcggatcgtg 1350 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

478924 segs, 333959956 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/USO7\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/2/pubpna/USO7\_PUBCOMB.seq:\*
3: /cgn2\_6/ptodata/2/pubpna/USO6\_NEW\_PUB.seq:\*
4: /cgn2\_6/ptodata/2/pubpna/USO6\_PUBCOMB.seq:\*
5: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\*
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11: /cgn2\_6/ptodata/2/pubpna/USO9\_PUBCOMB.seq:\*
12: /cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
13: /cgn2\_6/ptodata/2/pubpna/USO0\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO0\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/USO0\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score		Length	DB.	ID	Descrip
	:	1111				
-	444.8	32.9	1344	σ	US-10-077-870-1	Seguer
~	444.8	32.9	1344	10	US-09-825-923-1	ar wes
m	443	32.8	1353	σ	US-10-077-870-3	raima's
4	443	32.8	1353	10	US-09-825-923-3	o East
2	172.8	12.8	2482	σ	US-10-060-795B-10	raiman.
9	170.2	12.6	2625	σ	113-09-954-531-995	
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Gaps

72;

78 cccrractcccrecaggreacerreacecrectreecreecreecrecrecrecrecre 137

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Query Match 32.9%; Score 444.8; DB 9; Length 1344; Best Local Similarity 62.4%; Pred. No. 8e-78; Matches 820; Conservative 0; Mismatches 422; Indels 72;

138 CACCGIGITCGGCAACGIGCTCGTCATCACGCCGTGTTCACGAGCCGCGCGCTCAAGGC 197 

15 ccccracrocordedeccacacacacacaraccaccarcaccrrccrcarrerrr 74

317

257

135 CCTCAGAACCTGTTCCTGGTGTCGCTGGCCGCCGCCACTTGGTGGCCACGCTCAT 194

CATCCCTTTCTCGCTGGCCAACGAGGTCATGGGCTACTGGTACTTCGGCAAGGCTTGGTG

258

198 GCCCCAAAACCTCTTCCTGGTGTCTCTGGCCTCGGCCGACATCCTGGTGGCCACGCTCGT

Description	Sequence 1. Appli	Segmence 1 Appli	Segmence 3. Appli		Segmence 10 Appl	Segmence 995. App	Sequence 3. Appli	Segmence 3. Appli	Sequence 3. Appli	;		٠,	ī.	٠,		Semience 13. Appl			Sequence 6, Appli
ID	US-10-077-870-1	US-09-825-923-1	US-10-077-870-3	US-09-825-923-3	US-10-060-795B-10	US-09-954-531-995	US-09-349-755-3	US-09-166-334-3	US-09-350-206-3	US-09-349-755-1	US-09-166-334-1	US-09-350-206-1	US-10-185-991-1	US-10-005-010-1	US-09-864-761-3769	US-09-993-844-13	US-09-895-211-1	US-09-864-761-17258	US-09-349-755-6
DB	6	10	σ	70	σ	6	σ	σ	10	σ	σ	10	σ	12	10	10	10	10	σ
Query Match Length DB	1344	1344	1353	1353	2482	2625	1335	1335	1335	2689	2689	2689	2140	1645	1973.	1185	3683	694	1338
Query Match	32.9	32.9	32.8	32.8	12.8	12.6	12.4	12.4	12.4	12.4	12.4	12.4	11.2	10.9	10.9	10.5	10.5	10.4	10.4
Score	444.8	444.8	443	443	172.8	170.2	168	168	168	168	168	168	151.8	147.2	147.2	142	142	139.8	139.8
Result No.	-	7	m	4	ស	9	7	œ	6	10	11	12	13	14	c 15	16	17	18	19

Sequence 6, Appli	ø	m	Sequence 1, Appli			4	'n	7		Seguence 178, App	Sequence 12. Appl	٠,	7	214	Seguence 1598. Ap		Sequence 27, Appl	1, A	m	7	7	Seguence 9. Appli	'n	-	162
US-09-166-334-6	US-09-350-206-6	US-10-005-010-3	US-09-855-991A-1	US-09-349-755-4	US-09-166-334-4	US-09-350-206-4	US-10-185-991-5	US-09-993-844-12	US-10-185-991-3	US-09-822-830A-178	US-09-829-631A-12	US-09-993-844-9	US-09-811-286-1	US-09-954-456-214	US-09-954-456-1598	US-09-990-596-2	US-10-044-090-27	US-10-060-795B-1	US-09-897-006-34	US-10-060-795B-12	US-09-829-631A-7	US-09-829-631A-9	US-09-895-211-3	US-10-052-589-1	US-09-917-800A-1620
6	10	12	10	6	6	10	σ	10	σ	10	10	10	10	10	10	10	12	6	10	6	10	10	10	12	10
1338	1338	1690	1749	3244	3244	3244	1639	1356	1738	2173	1647	1113	3451	3451	3451	3451	3659	2455	9511	1248	1914	2108	3437	2048	2108
10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.0	10.0	7.6	9.7	9.4	9.3	9.3	9.3	9.3	9.3	9 .3	9.3	9.5	9.5	9.1	9.1	8.8	8.5	8.4
139.8	139.8	139.8	139.8	139.8	139.8	139.8	135	134.8	130.8	130.4	126.4	126	126	126	126	126	126	125.8	124.4	124.2	123	123	119.2	114.8	113.2
20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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General Information US/1007870

(Sequence 1, Application US/1007870

(BUREAL INFORMATION:

APPLICANT: Salonen, Jukka T

TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof

FILE REFERENCE: 0933-0183P

CURRENT APPLICATION NUMBER: US/10/077,870

CURRENT FILING DATE: 2002-05-21

FRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 3.1

LENGTH: 1344

TYPE: DNA

ORGANISM: Homo sapiens

FRATURE:

NAMENCEY: Coding sequence for variant human alpha-2B-adrenoceptor protein

US-10-077-870-1
RESULT 1
US-10-077-870-1
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APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: Abm colocule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1344
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COTHER INFORMATION: Coding sequence for variant human
COTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-913-1
                         Sequence 1, Application US/09825923 Patent No. US20010016338A1 GENERAL INFORMATION:
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Nyyss"nen, Kristiina
Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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Alhopuro, Pia
Karvonen, Matti
Koulu, Marku
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ORGANISM: Homo sapiens
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GACCTGGAGGAGGTCGTCTTCCGACCACGCCGAGGGGCCTCCAGGGCCCCGCAGACCC
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Best Local Similarity 63.3
Matches 837; Conservative
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                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)
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Publication No. US20030003470A1
GENERAL INFORMATION:
GENERAL Stalonen Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT PAPLICATION NUMBER: US/10/077,870
CURRENT FILIG DATE: 2002-05-21
FRIOR APPLICATION NUMBER: FI 20010323
FRIOR FILING DATE: 2001-02-20
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63.3%; Pred. No. 1.8e-77;
Live 0; Mismatches 405; Indels
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APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Ullamari
APPLICANT: Salonen, Jukka T
APPLICANT: Salonen, Jukka T
APPLICANT: Lakka, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Salonen, Riitta
APPLICANT: Walkonen, Well-Pekka
APPLICANT: Walkonen, Well-Pekka
APPLICANT: Walkonen, Vell-Pekka
APPLICANT: Walkonen, Vell-Pekka
APPLICANT: Walkonen, Well-Pekka
APPLICANT: Walkonen, Well-Pekka
APPLICANT: Walkonen, Well-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: A DNA molecule
CURRENT PELLORION NUMBER: US/09/0825,923
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-05-25
CURRENT PELCATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver: 2.1
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Patent No. US20010016338A1
GENERAL INFORMATION:
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Alhopuro, Pia
Karvonen, Matti
Koulu, Markku
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APPLICANT: Heinonen, Pa
APPLICANT: Alhopuro, Pi
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Length 1353;
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                                                                                                                                                                                                                                                                                             Sequence 10, Application US/10060795B

Publication No. US20030040022A1

GENERAL INFORMATION:

APPLICANT: Civelli Olivier

APPLICANT: Grandy, David K.

APPLICANT: Grandy, David K.

TITLE OF INVENTION: Dopamine Receptors and Genes
FILE REFERENCE: 90-1092-CCC

CURRENT APPLICATION NUMBER: US/10/60,795B

CURRENT APPLICATION NUMBER: 09/238977

PRIOR APPLICATION NUMBER: 09/238977

PRIOR APPLICATION NUMBER: 09/238977

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1989-11-18

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 10

LEGGTH: 2482
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ORGANISM: Homo sapiens
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,755
FILING DATE: 08-Jul-1999
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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COMPUTER READABLE FORM:
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US-09-349-755-3
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APPLICANT: Weaver. Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

TITLE OF INVENTION: Gene Sets

CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

SOFTWARE: PALENTING DATE: 2000-09-22

SEQ ID NOS: 1392

LENGTH: 2625
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Pred. No. 1.3e-24;
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US-09-954-531-995
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                                                                                                                                                                                                                                                                                                                                          63 CGGCGCCCGGGCCACCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCCGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09166334
Patent No. US20020168708A1
CENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1335,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: LAHIVE & COCKFIELD, LLP
28 State Street
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REFERENCE/DOCKET NUMBER: MNI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/166,33
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elizabeth A. Hanley REGISTRATION NUMBER: 33,5
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1335 base pairs
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STATE: Massachusetts
COUNTRY: USA
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STRANDEDNESS: single
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LOCATION:
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12.4%; Score 168; DB 9; Length 13
Best Local Similarity 51.4%; Pred. No. 3.2e-24;
Matches 440; Conservative 0; Mismatches 410; Indels
           APPLICATION NUMBER: US
FILING DATE: CURKONDS
APPLICATION NUMBER: US
FILING DATE: 04-DEC-1997
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFRENCE/DOCKET NUMBER: 33,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: US/09/042,780
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; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3
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12.4%; Score 168; DB 10; Length 1
Best Local Similarity 51.4%; Pred. No. 3.2e-24;
Matches 440; Conservative 0; Mismatches 410; Indels
                                                                                                             Version #1.25
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APPLICATION NUMBER: 09/042,780
FILIND DATE:
ATOMNEY AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33.505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEFAM. (6117)227-7400
TELEFAM. (6117)242-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER: IBM PC compatible OPERATING SYGTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/350,206 FILING DATE:
CLASSIFICATION:
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RESULT 11
US-09-166-334-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.4%; Score 168; DB 9; Length 2689; Best Local Similarity 51.4%; Pred. No. 3.5e-24; Matches 440; Conservative 0; Mismatches 410; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patent: Decode Ms.DoS
SOFTWARE: Patent: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,755
FILING DATE: 08-Jul-1999
CLASSIFICATION: «Unknown>
PROPLICATION NUMBER: US/09/042,780
FILING DATE: «Unknown>
FILING DATE: «Unknown>
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elizabeth A. Hanley
REGIGTNATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09349755
Patent No. US20020166131A1
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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US-09-349-755-1
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Patent No. US20020168708A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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480 CTCGGCCGTCATCTCCTGCCGCCGCTCATCTCCATCGAGAAGAAGGGCGGCGGCGGCGG
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Sequence 1, Application US/09350206
Patent No. US20020099199A1
GENERAL INFORMATION:
APPLICANT: AMERICAN D.J. Goodearl and Sandra Glucksman
APPLICANT: ADDRESS:
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFFWARE: PatentIn Release #1.0, Version #1.25
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURSTRING DATE:
CLASSIFICATION NUMBER: US/09/350,206
FILING DATE:
CLASSIFICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REFERENCA/COCKET NUMBER: MNI-032CP
REFERENCA/COCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2689 base pairs
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STRANDEDNESS: single
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291..1625
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NAME/KEY:
LOCATION:
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US-09-350-206-1
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12.4%; Score 168; DB 9; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.5e-24;
Matches 440; Conservative 0; Mismatches 410; Indels
                                                                                                                                                                           CDS
291..1625
                                                                                            Massachusetts
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MOLECULE TYPE: cDNA
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, LOCATION:
US-09-166-334-1
                                                                                                                                        COUNTRY:
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               TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TREAT BENIGN PROSTATIC HYPERPLASIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMINICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.2%; Score 151.8; DB 9; Best Local Similarity 51.9%; Pred. No. 4.7e-21; Matches 432; Conservative 0; Mismatches 377;
                                                                                                                                                                                                                                                                                                                                ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/185,991
FILING DATE: 28-Jun-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/444,783
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 1185 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 391-0525
TELEX: <Unknown>
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SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
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STRANDEDNESS: single
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                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                      SEQUENCES:
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                                                                               Length 2689;
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                                                                           Score 168; DB 10;
Pred. No. 3.5e-24;
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Publication No. US20030022900A1
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
                                                                           Query Match
Best Local Similarity 51.4%;
Matches 440; Conservative
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Best Local Similarity
US-09-350-206-1
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US-10-185-991-1
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FILING DATE: 2001-01-30
PPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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Sequence 1, Application US/10005010
SENERAL INFORMATION:
APPLICANT: Weinshank et al, Richard L.
TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
FILE REFERENCE: 36536-BA
CURRENT APPLICATION NUMBER: US/10/005,010
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/371,705
PRIOR PLILING DATE: 1999-08-09
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llarity 52.9%; Pred. No. 3.5e-20;
Conservative 0; Mismatches 298; Indels
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1645
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; LOCATION: (284)..(1414)
US-10-005-010-1
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US-09-864-761-3769/c
Sequence 3769, Application US/09864761
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Sequence 3769, Application US/09864761
SEREAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng C.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/622,366
PRIOR APPLICATION NUMBER: US/00-06-28
PRIOR PLILING DATE: 2000-09-36
PRIOR PLILING DATE: 2000-09-37
PRIOR PLILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US/09/864
PRIOR PLILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-10-30
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PRIOR PLILING DATE: 2000-10-30
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Best Local Similarity 52.9%; Pred. No. 3.6e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12;
                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FOTHER INFORMATION: MAP TO AL049576.15
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
COTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
US-09-864-761-3769
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-21

PRIOR FILING DATE: 2000-06-13

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOPTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 3769
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Search completed: March 11, 2003, 23:15:41 Job time : 1465.85 secs

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10-AUG-2000; 2
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1885.930 Million cell updates/sec
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15.1022/gcgdata/geneseqg-embl/NA1981.DAT; *
15.1022/gcgdata/geneseqg-embl/NA1982.DAT; *
15.1022/gcgdata/geneseqg-embl/NA1982.DAT; *
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18.1022/gcgdata/geneseqg-embl/NA2001.DAT; *
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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## ALIGNMENTS

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Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2AAR; GenBank Accession AF281308; chromosome 10; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "alpha-2AAR"
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..1353
/*tag= a
/product= "alpha-2AAF
     BP
                                                                                                                                                         Human alpha-2AAR encoding DNA
AAI99917 standard; DNA; 1350
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2000US-0636259.
2000US-0692077.
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                                                                                                                                                                                                                                                                           Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
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Matches 1350; Conservative
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P-PSDB; AAM52122.
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) obtaining a sample having a polymorphic site, comprising;

(a) obtaining a sample having a polymorphic site, comprising;

(b) detecting a polymorphic site comprising nucleotide positions 901-909

(c) (i), a site comprising cytosine or guanine at position 753 of (IIV)

or a site comprising cytosine or guanine at position 901-909

(c) or a site comprising cytosine or guanine at position 901-909

(d) or a site comprising cytosine or guanine at position 901-909

(d) or a site comprising cytosine or guanine at position 901-909

(d) or a site comprising cytosine or guanine at genotyphing an alpha2B, alpha2A or alpha2, comprising disease

(d) alpha2B, alpha2A or alpha2, comprising detecting a sescciated with alpha2B, alpha2A or alpha2, comprising detecting a golymorphic site which correlate to disease selected from cardiovascular compinations of these and individual's response compinations of these or alpha2C agonist (e.g. epinephrine, compinations of these or alterganist (e.g. epinephrine, diazoxan, tolazoline, guanabenz, WI4304, BHT933 and compinations of these or antergonist (e.g. yohimbine, prazosin, ARC 239, these by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate

C levels). The present sequence is that of the human alpha-2AAR variant
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                                                       Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic alte; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
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/*tag= a
/product= "alpha-2AAR"
replace(753,C)
/*tag= b
                    alpha-2AAR variant encoding DNA.
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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P-PSDB; AAM52123.
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Gaps

Score 1348.4; DB 23; Length 1350; Pred. No. 2.6e-203; 0; Mismatches 1; Indels 0; 0

99.08; 99.98;

Best Local Similarity 99.9 Matches 1349; Conservative

Query Match

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridiastion to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNR's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the
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ABQ47500 standard; DNA; 1733 BP XX
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Human; cytcsine methylation; 5'
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O1-SEP-2000; 2000DE-1043826.
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O1-SEP-2001; 2001WO-EP10074.
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O1-SEP-2000; 2000DE-1044543.
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O1-SEP-2000; 2000DE-1044543.
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O1-SEP-2000; 2000DE-1044566.
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methylation status of many C residues to be determined simultaneously. ABQ13410-ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                      Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
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1.3e-135;
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Pred. No. 1.3e-
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Best Local Similarity 80.0%;
Matches 1079; Conservative
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DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the rappeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method at a staus of many C residues to be determined simultaneously.

Ma013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                                                           Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic

Claim 12; 56pp + Sequence Listing; 56pp; German.

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
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                                                                                                                                               Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
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                                                                                                                                                                                                                                                                         Claim 1; Page 36-40; 190pp; English.
                                                     Berlin K;
                                               Piepenbrock C,
EPIGENOMICS
                                                                                                  WPI; 2002-154759/20
                                             Olek A,
(EPIG-)
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089
                           踞
                           ABQ47498 standard; DNA; 1733
                                                                             (first entry)
                                                                               12-JUL-2002
                                                    ABQ47498;
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RESULT 7
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (c) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic convert contains the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to both classes is determined from the cand the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ATCGTGCACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATCACACAGGCCATCGAG 420
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                                                                                                                                                                                                                                                                                                                Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                 Berlin K,
                                   01-SEP-2001; 2001WO-EP10074.
                                                                      01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                                                                                                               (EPIG-) EPIGENOMICS AG
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Matches 1030; Conserv
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TACAACCTGAAGCGCACGCCGCCGCATCAAGGCCATCATCATCACCGTGTGGGTCATC
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                                                                                                                                           TGCATCGGCTCCTTCTTCGCTCCTTGCTCATGATCCTGGTCTACGTGCGCATCTAC
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                                              TCGGCCGTCATCTCCCGCCGCTCATCTCCATCGAGAAGAAGGGCGGCGGCGGCGGCGGC
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Query Match 62.1
Best Local Similarity 76.3
Matches 1030; Conservative
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ABQ47499 standard; DNA; 1733
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12-JUL-2002 ABQ47499;

ABQ47499/c
ID ABQ47
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AC ABQ47
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DT 12-J1

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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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     Oligonucleotide for detecting cytosine methylation SEQ
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                                                               WO200218632-A2
                                                   Homo sapiens
                                                                             07-MAR-2002
                                                                                                                                       olek A,
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useful of Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic correct

Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;

ö 1414 1354 1294 240 180 GGCGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCTGGCC 120 Gaps 9 1473 ATGGGTTTTTTGTAGTCGGACGCGCGTAACGCGATGGAACGGGATCGAGCGTCGGG GGTTTGTTTATGTTTATCGTGTTCGGTAACGTGTTCGTTATTATCGTCGTGTTACG 1 ATGGCCTCCCTGCAGCCGGACGCGGGCAACGCGAACGGGACCGAGGCCCCGGGG 1413 GCCGCCTTCGGGTTATTTTTTTTTTTGTAGGTCACGTTGACGTTGGTGTTTTGGTC GGCCTGCTCATGCTGCTCACCGTGTTCGGCAACGTGCTCGTCATCATCATCACCTGTTCACG ; 0 Length 1733; Indels Score 838; DB 24; 1 Pred. No. 3.2e-123; 0; Mismatches 320;

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; addisease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                       system disease; cytosine methylation; antiasthmatic;
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1321 CTCTGTCGGGGGGACAGGAAGCGGATCGTG
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                                                                                                                                                                                                                                                                                                                                                   adrenergicalpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia; drug abuse; migraine; ds.
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.larity 76.3%; Pred. No. 2.9e-123;
Conservative 0; Mismatches 320; Indels 0
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polymorphic site; allelic variant, cardiovascular disease;
central nervous system disease; adenylyl cyclase; MAP kinase activity;
phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
                                                                                                                                                                              1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "alpha-2CAR"
/note= "sequence includes a 12 nucleotide polymorphic
site at nucleotides 961-972 absent in the
alpha-2CAR variant (AA199933)"
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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P-PSDB; AAM52124.
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cappage and the part of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, quanaberi, VK43AQ, BHT933 and combinations of these) or antegonist (e.g. yohimbine, prazosin, ARC 239, these) by detecting the polymorphic site and combinations of these by detecting the polymorphic site and correlated to adenylyl cycdetermined response (where the response is correlated to adenylyl cyclese, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2CAR, the sequence includes a 12 mucleotides polymorphic site at nucleotides

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/product= "alpha-2CAR"
/note= "sequence is deleted for a 12 nucleotide
/note= "sequence is deleted for a 19 nucleotide
polymorphic site at nucleotides 961-972
wildtype sequence (AAI99931)"
Human alpha-2CAR variant encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site encoding an alpha-2B, alpha-2D or alpha-2C or fragment or complement of; and catching a polymorphic site comprising cytosine or guanine at positions 901-909 of (I), a site comprising cytosine or guanine at positions 901-909 of or a site comprising cytosine or guanine at position 53 of (IIV) or a site comprising cytosine or (B) degegogorgap and (III). The method may be used for genotyping an appha-2B, alpha-2A or alpha-2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease comprehent of site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response compinations of these or alpha-2C agonist (e.g. sphimphrine combinations of these or antagonist (e.g. sphimphrine hypotherior indine, cardiovascular combinations of these or antagonist (e.g. sphimphrine hypotherior indine, polymorphic site and correlating the site to a predetermined response (where the response is correlating the site to a predetermined response (where the response is correlating the site to a predetermined response correlating the site of levels). The present sequence is that of the human alpha-2CAR variant, corrected solls as why he present sequence is that of the human alpha-2CAR variant, corrected solls and correlating the site at the sequence is deleted for a 12 nucleotide polymorphic site at the correlating the site at the correlating the sequence is elected for a 12 nucleotide polymorphic site at the correlating the site at the correlation of the sequence is deleted for a 12 nucleotide polymorphic site at the correlating the site at the correlating the site at the correlation of the sequence is correlated to adenty the sequence is correlated to adenty the correlati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
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Pred. No. 6.2e-73;
0; Mismatches 414; Indels
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                              17-APR-2001; 2001WO-US12575
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Matches 870; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; therapy; vascular contraction; variant; coronary artery; coronary hat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                   Pesonen U;
       GICATCTACACCATCTICAACCACGATTICCGCCGCGCTTCAAGAAGAICCTCTGTCGG 1329
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/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Scheinin M, Salonen JT,
Salonen R, Kauhanen J,
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cc receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) obtaining a sample having a polymucleotide encoding an alpha-2B,

(a) black or alpha2C or fragment or complement of; and

(b) detecting a polymorphic site comprising nucleotide positions 901-909

CC (I), a site comprising cytosine or guanine at position 753 of (IIV)

CC or a site comprising cytosine or guanine at position 753 of (IIV)

CC positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, constingue may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, constingue may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, dazoxan, tolazoline, phentolamine and combinations of these) or antagonist (e.g. yohimbine prazosin, ARC 239, crawolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlating the site to a predetermined response extivity, phosphorylation or inositol phosphate (cyclebal). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide cyclebal.
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                                        738 CGAGCGCAGGCCCCAACGGTCTGGGCCCCCGAGCGCGCGGGGCCCCGGGG-----GGGCGCA 792
                                                                      664 caaccargargagactrragctrcagccaactgccagccragaccrcragagr 723
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Scoring table:

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Perfect score:

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Sequence 21, Sequence 21, Sequence 21, Sequence 21, Sequence 21, Sequence 8, A Sequence 6, A Sequence 3, A Sequence 3, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Sequence 27, A Seque
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                                                         Sequence
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ADDRESSEE: CESTRAAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: POPPOS/MS-DOS
SOFTWARE: Date of the compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN NUMBER: US/07/676,174A
FILING DATE: 19910328
ATTORNEY/AGENT INFORMATION:
NAME: SCOCKT WAS SON T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION INFORMATION:
TELEPHAK: (202)861-3000
TELEFRAK: (202)861-3000
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                    US-08-08-772A-114
US-08-087-772A-114
US-08-450-96-1
US-08-66-051-5
US-08-928-611-21
US-09-928-611-21
US-09-938-074-21
US-09-131-553-8
US-08-131-553-8
US-08-131-553-8
US-08-14-138-7
US-09-165-543-6
US-08-165-543-4
US-08-165-543-4
US-08-125-001-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07676174A
Patent No. 534476
GENERAL INFORMATION:
APPLICAMT: Ventor, J. Craig
TITLE OF INVENTION: Octopamine rece
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)822-8944
TELEFAX: (714627 CUSH
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3335 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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Best Local Similarity
Matches 352; Conserv
TOPOLOGY:
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LOCATION:
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Sequence 1, Al
Sequence 13,
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Sequence 5, Al
Sequence 15,
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Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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S-09-642-855-5
S-09-642-514-5
S-08-475-742-15
S-08-334-698-1
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US-09-688-415-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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247
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                                                                                                                           308 AGGCTTGGTGCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCGTCGTGC 367
                   ACCTGTGTGTGCCTAGGCCCTCGACCGGTACTGGGCCATTACGGACCCCCATCAACTATGCCC
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CGCTCAAGGCGCCCCAAAACCTCTTCCTGGTGTCTCTGGCCTCGGCCGACATCCTGGTGG
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Patent No. 5885893
BENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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STREET: 28 State Street
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REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STREET: Massachusetts
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APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAMME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
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51.4%; Pred. No. 3e-22;
ive 0; Mismatches 410; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMINICATION INFORMATION:
TELEPAN: (617)227-7400
TELEPAN: (617)227-7400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
LENGTH: 1335 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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Matches 440; Conservative
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MEDIUM TYPE: Floppy
                                            837 GCCCGCGCCGGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
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; LOCATION:
US-09-165-543-3
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12.4%; Score 168; DB 3; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.2e-22;
Matches 440; Conservative 0; Mismatches 410; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09165543
Patent No. 6093545
PARENT NO. 6093545
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION:
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/165,543 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elizabeth A. Hanley
REGISTRATION UNUMBER: 33.505
REFERENCA/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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STATE: Massachusetts
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LOCATION:
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US-09-165-543-1
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    REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCS CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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291..1625
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MOLECULE TYPE: cDNA
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nes 440; Conserv
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, LOCATION:
US-08-985-090-1
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US-09-642-855-6
Sequence 6, Application US/09642855
Fatent No. 6413743
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Briander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pivat, Arne
APPLICANT: Burner, Arne
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Elander, Mark
APPLICANT: Huvar, Arne
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
TITLE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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US-09-167-354-6
Sequence 6, Application US/09167354A
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APPLICANT: Lovenberg, Timothy
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CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION UNBER: 09/167,354
PRIOR RPLING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFURARE: Patentin Ver. 2.0
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APPLICANT: Erlander, Mark
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Hyava: Arne
TITLE OF INVENTION: DUB ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT PILING DATE: 2000-08-21
PRIOR PPLICATION NUMBER: US 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOTTWARE: Patentin Ver. 2.0
SEQ ID NO 6
SEQ ID NO 6
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12.3%; Score 166.4;
Best Local Similarity 51.3%; Pred. No. 5.8e
Matches 439; Conservative 0; Mismatches
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Patent No. 6437100
GENERAL INFORMATION:
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                   CGGCAAGGCTTGGTGCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCCAT 362
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; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Friander, Mark
; APPLICANT: Payet, Jayashree
; TITLE OF INVENTION: SUBTYPE
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR PELICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
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US-09-642-855-5
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US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
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APPLICANT: Lovenberg, Timothy
APPLICANT: Evlander, Mark
APPLICANT: Pyati, Jayaahree
APPLICANT: Pyati, Jayaahree
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
LENGTH: 2699
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US-09-167-354-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-167-354-5
Sequence 5, Application US/09167354A
; Patent No. 613659
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ORGANISM: Artificial Sequence
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Exlander, Mark
APPLICANT: Friander, Arne
APPLICANT: Huvar, Arne
TITLE OF INVENTION: BUBTYPE
TITLE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 2000-08-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: CDNAUS-09-642-514-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
12.3%; Score 166.4; DB 4;
Best Local Similarity 51.3%; Pred. No. 6.3e-22;
Matches 439; Conservative 0; Mismatches 411;
                                      09/167,354
PRIOR APPLICATION NUMBER: US 09, PRIOR FILING DATE: 1998-10-06 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 5; LENGTH: 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: JOINTH A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: GOOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
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Patent No. 5556753
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                        RESULT 12
US-08-475-742-15
Sequence 15, Application US/08475742
Fatern No. 6121015
GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1995-06-07
EARLIER PPLICATION NUMBER: US 08/261,293
EARLIER PPLICATION NUMBER: US 08/261,293
EARLIER PPLICATION NUMBER: US 08/014,013
SEARLIER PLING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 15
LENGTH: 2428
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TYPE: DNA
ORGANISM: CDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(2428)
OTHER INFORMATION: Rat d2 receptor sequence
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1144 AGGCGCTGAGGCCGGG 1159
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VOLUME: 336
PAGES: 783-787
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APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Thareas A. Branchek, John M. Werzel and Paul R. Hartig
APPLICANT: Thereas A. Branchek, John M. Werzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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909 CITCIGCGGIAICACCGAGGAGGCGGGCIACGCTGTCTTCTCCTCCGTGTGTGTCTTTA 968
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Pred. No. 2.6e-19;
0; Mismatches 377;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/ACTION: 514
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 64-655
TELEPHONE: (212) 64-655
TELEPHONE: (212) 42553 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 644-0526
TELEFAK: (212) 644-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                       SUFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
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US-08-334-698-1
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APPLICANT: Jonathan A. Bard et al.
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: GOOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
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STATE: New York
COUNTRY: U.S.A.
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Pred. No. 2.6e-19;
0; Mismatches 377;
                            COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTATION NUMBER: 28,678
RECISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER SILES:
CROUNT COMPUTER SILES:
COMPUTER: ALL STATEMENT OF SEQUENCE CHARACTER SILES:
COMPUTER: ALL STATEMENT OF SEQUENCE CHARACTER SILES:
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Best Local Similarity 51.9%;
Matches 432; Conservative
Floppy disk
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STRANDEDNESS: single
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OTHER INFORMATION:
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ANTI-SENSE: N
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<sup>1029</sup> CACGCGCAGCCTCGAGGCGAGGCAAGGCGAGGCAAGGCCTCCGAGGTGCT 1088 672 GCGTCGCACCCGCGTGCCACCCAGCCGCCGGGGTCCGGACGCCGTCGCCGCGCGGGG 731 q ò ò

Search completed: March 11, 2003, 07:41:17 Job time : 108.111 secs

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<sup>65</sup> dg